GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 1, 2005, 00:42:12 ; Search time 529 Seconds
(without alignments)
10306.378 Million cell updates/sec

Title: US-09-964-277-20
Perfect score: 3332
Sequence: 1 gagagaaggagaagataata.....ataaagatgaacttggtttc 3332

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2950	88.5	3544	4	US-09-816-494-1	Sequence 1, Appli
2	1660	49.8	1998	4	US-09-816-494-3	Sequence 3, Appli
3	294.6	8.8	333	4	US-09-513-999C-2877	Sequence 2877, Ap
4	247	7.4	279	4	US-09-016-434-91	Sequence 91, Appl
5	225.2	6.8	2377	4	US-09-920-668-3	Sequence 3, Appli
6	223.6	6.7	2351	4	US-09-949-016-3250	Sequence 3250, Ap
c 7	187.8	5.6	378	4	US-09-513-999C-3684	Sequence 3684, Ap
8	109.6	3.3	1830	4	US-09-557-921-1	Sequence 1, Appli
9	95	2.9	2283	4	US-09-949-016-4617	Sequence 4617, Ap
10	95	2.9	2303	4	US-09-922-146-3	Sequence 3, Appli
11	94.6	2.8	1208	4	US-09-023-655-347	Sequence 347, App
12	90.2	2.7	2109	4	US-09-016-434-1135	Sequence 1135, Ap
13	90.2	2.7	2109	4	US-09-023-655-946	Sequence 946, App
14	90.2	2.7	2475	4	US-09-949-016-2615	Sequence 2615, Ap
15	89.2	2.7	13782	4	US-09-949-016-14992	Sequence 14992, A
16	86.2	2.6	240	4	US-09-016-434-776	Sequence 776, App
17	85.6	2.6	1619	4	US-09-702-705-801	Sequence 801, App
18	85.6	2.6	1619	4	US-09-736-457-801	Sequence 801, App
19	85.6	2.6	1619	4	US-09-614-124B-801	Sequence 801, App
20	85.6	2.6	1619	4	US-09-671-325-801	Sequence 801, App
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22	85.6	2.6	1619	4	US-09-658-824-801	Sequence 801, App
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27	85.6	2.6	4637	4	US-09-589-184-804	Sequence 804, App
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45	84	2.5	2109	4	US-09-671-325-826	Sequence 826, App

ALIGNMENTS

RESULT 1
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2583)
US-09-816-494-1

Query Match 88.5%; Score 2950; DB 4; Length 3544;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;

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Qy      197 GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATG 256
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Qy        927 ---------------------------------------------------------- 926

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Qy        927 ----------------------------------------------------------AGGAGC 932
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Qy       2013 GGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATT 2072
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Qy       2793 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCC 2852
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Qy       2853 TAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACC 2912
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Db       3463 AATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3522
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RESULT 2
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494-3

Query Match 49.8%; Score 1660; DB 4; Length 1998;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1834; Conservative 0; Mismatches 0; Indels 164; Gaps 1;

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Qy        562 ATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGCTGGAA 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGCTGGAA 60

Qy        622 AGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATACATCC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATACATCC 120

Qy        682 CACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGCAACAG 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGCAACAG 180

Qy        742 GACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACATTGAT 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACATTGAT 240

Qy        802 TGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCTCTTCA 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCTCTTCA 300

Qy        862 GACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTCACCTG 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTCACCTG 360

Qy        922 CTTGC---------------------------------------------------------- 926
              |||||
Db        361 CTTGCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAAAATCC 420

Qy        927 ---------------------------------------------------------------- 926

Db        421 ACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGCCAACC 480

Qy        927 ----------------------------------------------------AGGAGCTGATG 937
                                                                   ||||||||||||
Db        481 CGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGGAGCTGATG 540

Qy        938 CAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTT 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTT 600

Qy        998 ATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 660

Qy       1058 CCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTT 1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTT 720

Qy       1118 CTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATG 1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATG 780

Qy       1178 AAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACT 1237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACT 840

Qy       1238 ATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAAC 1297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAAC 900

Qy       1298 CAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGCCAAAT 1357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGCCAAAT 960

Qy       1358 GAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTCCACCC 1417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTCCACCC 1020
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Qy       1418 TGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCAGCGTG 1477
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCAGCGTG 1080

Qy       1478 CCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTC 1537
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTC 1140

Qy       1538 AGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTC 1597
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTC 1200

Qy       1598 TCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATGGCTTC 1657
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATGGCTTC 1260

Qy       1658 TCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGACCAAC 1717
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGACCAAC 1320

Qy       1718 AAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCAGTCCT 1777
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCAGTCCT 1380

Qy       1778 GATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACAGCCAG 1837
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACAGCCAG 1440

Qy       1838 AGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCCTTTTA 1897
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCCTTTTA 1500

Qy       1898 TCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTTTCGGC 1957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTTTCGGC 1560

Qy       1958 CTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCTGGCAC 2017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCTGGCAC 1620

Qy       2018 TCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATTTTGCC 2077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATTTTGCC 1680

Qy       2078 ACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTTACTCT 2137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTTACTCT 1740

Qy       2138 GCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCAGGCGG 2197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCAGGCGG 1800

Qy       2198 CAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCTTTGAA 2257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCTTTGAA 1860

Qy       2258 AAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAGAGAAC 2317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 AAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAGAGAAC 1920

Qy       2318 AGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAA 2377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAA 1980

Qy       2378 ATCATTGAGGTCTCCTGA 2395
             ||||||||||||||||||
Db       1981 ATCATTGAGGTCTCCTGA 1998


RESULT 3
US-09-513-999C-2877
; Sequence 2877, Application US/09513999C
; Patent No. 6783961
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```
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 2877
;   LENGTH: 333
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 127..333
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 17
;   OTHER INFORMATION: h=a or c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 18
;   OTHER INFORMATION: y=c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 19
;   OTHER INFORMATION: k=g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 36
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 58
;   OTHER INFORMATION: r=a or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 237
;   OTHER INFORMATION: w=a or t
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 37
;   OTHER INFORMATION: Xaa=His or Gln
US-09-513-999C-2877

  Query Match             8.8%;  Score 294.6;  DB 4;  Length 333;
  Best Local Similarity   97.3%;  Pred. No. 2.1e-82;
  Matches  326;  Conservative    5;  Mismatches    0;  Indels    4;  Gaps    3;

Qy        595 ACTGAGAGGTTGGTGGCTCTGCTGGAAAGTGGAACGG-AAAAAGTGCTGCTAATTGATAG 653
              ||||||||||||||::  :|||||||||||||||| ||||||||||||||||||||||:
Db          1 ACTGAGAGGTTGGTGGHY--KCTGGAAAGTGGAACGGNAAAAAGTGCTGCTAATTGATAR 58

Qy        654 CCGGCCATTTGTGGAATA-CAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCT 712
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         59 CCGGCCATTTGTGGAATACCAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCT 118

Qy        713 CCAAGCTTATGAAGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGC 772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 CCAAGCTTATGAAGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGC 178

Qy        773 ATTCAGCGAAACATAAGGTTGACATTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAA 832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        179 ATTCAGCGAAACATAAGGTTGACATTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAWA 238

Qy        833 GCTCCCAAGATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAAC 892
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 GCTCCCAAGATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAAC 298
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Qy        893 TGGAGAAGAGCTTCAACTCTGTTCACCTGCTTGCA 927
              |||||||||||||||||||||||||||||||||||
Db        299 TGGAGAAGAGCTTCAACTCTGTTCACCTGCTTGCA 333
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RESULT 4
US-09-016-434-91
; Sequence 91, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 279 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGFET03
; CLONE: 1234795
US-09-016-434-91

Query Match 7.4%; Score 247; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.2e-67;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        538 GGGAAAAGAGGACTTATTGTTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACT 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGAAAAGAGGACTTATTGTTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACT 60

Qy        598 GAGAGGTTGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGG 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGAGGTTGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGG 120

Qy        658 CCATTTGTGGAATACAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAG 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCATTTGTGGAATACAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAG 180

Qy        718 CTTATGAAGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCA 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTATGAAGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCA 240
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Qy        778 GCGAAAC 784
              |||||||
Db        241 GCGAAAC 247
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RESULT 5
US-09-920-668-3
; Sequence 3, Application US/09920668
; Patent No. 6482644
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsert
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
; FILE REFERENCE: RTS-0246
; CURRENT APPLICATION NUMBER: US/09/920,668
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)...(2012)
US-09-920-668-3

Query Match 6.8%; Score 225.2; DB 4; Length 2377;
Best Local Similarity 60.6%; Pred. No. 9.9e-60;
Matches 418; Conservative 0; Mismatches 248; Indels 24; Gaps 2;

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Qy        927 AGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAA 986
              |||| ||||||  ||| ||||| ||  | || ||  | || ||||||||  |||| || |
Db        670 AGGATCTGATGACGCAAAATGGAATAAGCTACGTCCTCAACGCCAGCAACTCCTGCCCCA 729

Qy        987 AGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTG 1046
              |||||||||| |||  ||||   |  ||| |||| || ||  | || |||| ||  ||||
Db        730 AGCCTGACTTCATCTGCGAGAGCCGCTTCATGCGGGTCCCCATCAACGACAACTACTGTG 789

Qy        1047 AGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCA 1106
               | ||| |  |||| ||| |||||||  ||  | || |||| || |||||  ||   |||||
Db         790 AAAAACTGCTGCCCTGGCTGGACAAGTCCATCGAGTTCATCGATAAAGCCAAGCTCTCCA 849

Qy        1107 ATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCG 1166
               |    ||  | || |||||| | ||||| |||||||||||| |||||||||||| ||||
Db         850 GCTGCCAAGTCATCGTCCACTGTCTGGCTGGCATCTCCCGCTCTGCCACCATCGCCATCG 909

Qy        1167 CCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAA 1226
               |||||||||||||||  |||| ||||||  |  || || ||||| || ||||| || |
Db         910 CCTACATCATGAAGACCATGGGCATGTCCTCCGACGACGCCTACAGGTTCGTGAAGGACA 969

Qy        1227 AAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGA 1286
               | ||  | || || || |||||||| || |||||||| || ||||| || |||   |
Db         970 GGCGCCCGTCCATCTCGCCCAACTTCAACTTCCTGGGCCAGCTGCTGGAGTACGAGCGCA 1029

Qy        1287 AGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGG 1346
               | | |||   | | | |          ||       | |||  | |     | |   | ||
Db        1030 CGCTGAAGCTGCTGGCCGCCCTGCAGGGCGACCCGGGCACCCCCTCAGGGACG---CCGG 1086

Qy        1347 AGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCC 1406
               ||   ||       |||| | | |  | | |    | | |  |      ||  |
Db        1087 AGCCTCCGCCCAGTCCTGCCGCCGGGGCCCCGCTGCCACGGCTGCCACCACCTACCTCAG 1146

Qy        1407 TCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATC 1466
               ||  |  ||   |  | ||| ||  ||||  |
Db        1147 AGAGCGCTGCCACAGGGAATGCGGCTGCCAGGGAGGGCG---------------------- 1185

Qy        1467 CCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGG 1526
               |   |||| |  | | | ||||  || ||  ||  |||      | |  |||| | |||
Db        1186 GCCTGAGCGCGGGCGGGGAGCCCCCCGCGCCCCCCACGCCCCCGGCGACCAGCGCACTGC 1245

Qy        1527 TACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCA 1586
               ||||  ||  | || |||||||| ||| | ||| | ||| | ||||  ||    ||||
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Db       1246 AGCAGGGCCTGCGCGGCCTGCACCTCTCCTCGGACCGCCTGCAGGACACTAACCGCCTCA 1305

Qy       1587 AGCGTTCCTTCTCTCTGGATATCAAATCAG 1616
              |||| |||||||| ||||| ||||| || |
Db       1306 AGCGCTCCTTCTCCCTGGACATCAAGTCTG 1335


RESULT 6
US-09-949-016-3250
; Sequence 3250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3250
;   LENGTH: 2351
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-3250

  Query Match             6.7%;  Score 223.6;  DB 4;  Length 2351;
  Best Local Similarity   60.4%;  Pred. No. 3.2e-59;
  Matches  417;  Conservative    0;  Mismatches  249;  Indels   24;  Gaps    2;

Qy        927 AGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAA 986
              |||| ||||||  ||| ||||| ||  | || ||  | || ||||||||  |||| || |
Db        644 AGGATCTGATGACGCAAAATGGAATAAGCTACGTCCTCAACGCCAGCAACTCCTGCCCCA 703

Qy        987 AGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTG 1046
              |||||||||| ||| |||| |  ||| |||| || ||  | || |||| ||  ||||
Db        704 AGCCTGACTTCATCTGCGAGAGCCGCTTCATGCGGGTCCCCATCAACGACAACTACTGTG 763

Qy       1047 AGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCA 1106
              | ||| |  |||| ||| ||||||| ||  | || ||||| || ||||| ||   |||||
Db        764 AAAAACTGCTGCCCTGGCTGGACAAGTCCATCGAGTTCATCGATAAAGCCAAGCTCTCCA 823

Qy       1107 ATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCG 1166
                |   ||  | || |||||| | ||||| |||||||||| |||||||||| ||||
Db        824 GCTGCCAAGTCATCGTCCACTGTCTGGCTGGCATCTCCCGCTCTGCCACCATCGCCATCG 883

Qy       1167 CCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAA 1226
              |||||||||||||||  |||| |||||| |  || || || ||||| || ||||| || |
Db        884 CCTACATCATGAAGACCATGGGCATGTCCTCCGACGACGCCTACAGGTTCGTGAAGGACA 943

Qy       1227 AAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGA 1286
                | ||  | || || || |||||||| || |||||||| || ||||| || |||   |
Db        944 GGCGCCCGTCCATCTCGCCCAACTTCAACTTCCTGGGCCAGCTGCTGGAGTACGAGCGCA 1003

Qy       1287 AGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGG 1346
                | |||  | | | |              ||     | |||                | | |
Db       1004 GCCTGAAGCTGCTGGCCGCCCTGCAGGGCGACCCGGGCA----------CCCCCTCAG 1051

Qy       1347 AGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCC 1406
              || |||  |    ||   |  | ||| | | | ||     | |  | |   | | || |
Db       1052 GGACGCCGGAGCCTCCGCCCAGTCCTGCCGCCGGGGCCCCGCTGCCACGGCTGCCACCAC 1111

Qy       1407 TCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATC 1466
                |   ||    | || | | | |  |  | |  ||    |      | |
Db       1112 CTACCTCAGAGAGCGCTGCCACAGGGAATGCGGCTGCCAGGGAGGGCGGCCTG------- 1164

Qy       1467 CCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGG 1526
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                |||| |  | | | ||||  || ||  ||  |||     | |  |||| | |||
Db       1165 -----AGCGCGGGCGGGGAGCCCCCCGCGCCCCCCACGCCCCCGGCGACCAGCGCACTGC 1219

Qy       1527 TACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCA 1586
                ||||  ||  | || |||||||| ||| | ||| | ||| | |||| ||    ||||
Db       1220 AGCAGGGCCTGCGCGGCCTGCACCTCTCCTCGGACCGCCTGCAGGACACTAACCGCCTCA 1279

Qy       1587 AGCGTTCCTTCTCTCTGGATATCAAATCAG 1616
              |||| |||||||| ||||| ||||| || |
Db       1280 AGCGCTCCTTCTCCCTGGACATCAAGTCTG 1309


RESULT 7
US-09-513-999C-3684/c
; Sequence 3684, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 3684
;   LENGTH: 378
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 216..377
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 164
;   OTHER INFORMATION: k=g or t
US-09-513-999C-3684

  Query Match             5.6%;  Score 187.8;  DB 4;  Length 378;
  Best Local Similarity   99.0%;  Pred. No. 1.7e-48;
  Matches  189;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        605 TGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTG 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 TGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTG 319

Qy        665 TGGAATACAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGA 724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TGGAATACAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGA 259

Qy        725 AGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAAC 784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 AGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAAC 199

Qy        785 ATAAGGTTGAC 795
              |||||||  ||
Db        198 ATAAGGTAAAC 188


RESULT 8
US-09-557-921-1
; Sequence 1, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-10 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.416
;  CURRENT APPLICATION NUMBER: US/09/557,921
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;  CURRENT FILING DATE:  2000-04-20
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-557-921-1

  Query Match             3.3%;  Score 109.6;  DB 4;  Length 1830;
  Best Local Similarity   61.0%;  Pred. No. 3.6e-23;
  Matches  178;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

Qy       1006 GTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCGTGGTT 1065
             ||   | | |  |||  |||| |  | |||||||       ||||  |   || ||  ||
Db       1187 GTTCAACTACAAGCGGCTGCCAGCCACTGACAGCAACAAGCAGAACCTGCGGCAGTACTT 1246

Qy       1066 GGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTAGTGCA 1125
              ||  |  |  | || |||||||| ||||  |     |          |  ||||  | ||
Db       1247 TGAAGAGGCTTTTGAGTTCATTGAGGAAGCTCACCAGTGTGGGAAGGGGCTTCTCATCCA 1306

Qy       1126 CTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGGAT 1185
              |||    |||||| | ||||||||||||||||||||  |||||  |||  | ||||||    |
Db       1307 CTGCCAGGCTGGGGTGTCCCGCTCCGCCACCATCGTCATCGCTTACTTGATGAAGCACAC 1366

Qy       1186 GGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATATCTCC 1245
                 ||| |  |   ||| |||||  | ||||||  ||||  |||  ||||  | |||  || ||
Db       1367 TCGGATGACCATGACTGATGCTTATAAATTTGTCAAAGGCAAACGACCAATTATCTCCCC 1426

Qy       1246 AAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAAC 1297
              ||||  |  ||  ||  ||||  ||   |  ||  ||  |   |||  |   |  |  ||  |||
Db       1427 AAACCTTAACTTCATGGGGCAGTTGCTAGAGTTCGAGGAAGACCTAAACAAC 1478


RESULT 9
US-09-949-016-4617
; Sequence 4617, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4617
;   LENGTH: 2283
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-4617

  Query Match             2.9%;  Score 95;  DB 4;  Length 2283;
  Best Local Similarity   58.8%;  Pred. No. 1.8e-18;
  Matches  164;  Conservative    0;  Mismatches  115;  Indels    0;  Gaps    0;

Qy       1004 GAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCGTGG 1063
             || | ||| | |  ||   | ||  |   |||  ||   |  ||||  | | || ||
Db        858 GACTTTCACTACAAGCAGATCCCCATCTCCGACCACTGGAGCCAGAACCTGTCGCGGTTC 917

Qy       1064 TTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTAGTG 1123
              ||      |  |  | || ||||||||  | ||     ||   ||  |  | || || ||
Db        918 TTTCCGGAGGCCATTGAGTTCATTGATGAGGCCTTGTCCCAGAACTGCGGGGTGCTCGTC 977

Qy       1124 CACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGG 1183
              ||||| || || ||| ||  ||| || | |||| || || | |||||| ||||| ||| |
Db        978 CACTGCTTGGCGGGGGTCAGCCGTTCTGTCACCGTCACTGTGGCCTACCTCATGCAGAAG 1037

Qy       1184 ATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATATCT 1243
              |  || | ||| |  | || || ||      | || ||    || |   ||| || ||
Db       1038 CTCCACCTCTCTCTCAACGATGCCTATGACCTGGTCAAGAGGAAGAAGTCTAACATCTCC 1097

Qy       1244 CCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAG 1282
              || |||||||| ||  |||| ||  | |||||| ||||
Db       1098 CCCAACTTCAACTTCATGGGGCAGTTGCTGGACTTTGAG 1136


RESULT 10
US-09-922-146-3
; Sequence 3, Application US/09922146
; Patent No. 6566133
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Brett P. Monia
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
;  FILE REFERENCE: RTS-0252
;  CURRENT APPLICATION NUMBER: US/09/922,146
;  CURRENT FILING DATE:  2001-08-01
;  NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
;   LENGTH: 2303
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (114)...(1268)
US-09-922-146-3

  Query Match             2.9%;  Score 95;  DB 4;  Length 2303;
  Best Local Similarity   58.8%;  Pred. No. 1.8e-18;
  Matches  164;  Conservative    0;  Mismatches  115;  Indels    0;  Gaps    0;

Qy       1004 GAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCGTGG 1063
             || | ||| | |  ||   | ||  |   |||  ||   |  ||||  | | || ||
Db        858 GACTTTCACTACAAGCAGATCCCCATCTCCGACCACTGGAGCCAGAACCTGTCGCGGTTC 917

Qy       1064 TTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTAGTG 1123
              ||      |  |  | || ||||||||  | ||     ||   ||  |  | || || ||
Db        918 TTTCCGGAGGCCATTGAGTTCATTGATGAGGCCTTGTCCCAGAACTGCGGGGTGCTCGTC 977

Qy       1124 CACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGG 1183
              ||||| || || ||| ||  ||| || | |||| || || | |||||| ||||| ||| |
Db        978 CACTGCTTGGCGGGGGTCAGCCGTTCTGTCACCGTCACTGTGGCCTACCTCATGCAGAAG 1037

Qy       1184 ATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATATCT 1243
              |  || | ||| |  | || || ||      | || ||    || |   ||| || ||
Db       1038 CTCCACCTCTCTCTCAACGATGCCTATGACCTGGTCAAGAGGAAGAAGTCTAACATCTCC 1097

Qy       1244 CCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAG 1282
              || |||||||| ||  |||| ||  | |||||| ||||
Db       1098 CCCAACTTCAACTTCATGGGGCAGTTGCTGGACTTTGAG 1136


RESULT 11
US-09-023-655-347
; Sequence 347, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
```

```
;       COUNTRY:  USA
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/023,655
;       FILING DATE:  HEREWITH
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Zeller, Karen J.
;       REGISTRATION NUMBER:  37,071
;       REFERENCE/DOCKET NUMBER:  PA-0001 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (650) 855-0555
;       TELEFAX:  (650) 845-4166
;   INFORMATION FOR SEQ ID NO:  347:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1208 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       LIBRARY:  THYRNOT03
;       CLONE:  1444245
US-09-023-655-347

  Query Match             2.8%;  Score 94.6;  DB 4;  Length 1208;
  Best Local Similarity   64.3%;  Pred. No. 1.5e-18;
  Matches  142;  Conservative    0;  Mismatches   79;  Indels    0;  Gaps    0;

Qy       1077 TAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTG 1136
              | || |||||||||| ||||  |     |          |  |||||  | |||||    ||||
Db          4 TTGAGTTCATTGAGGAAGCTCACCAGTGTGGGAAGGGGCTTCTCATCCACTGCCAGGCTG 63

Qy       1137 GGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTT 1196
              || | ||||||||||||||||||  ||||| ||| | ||||||   |     ||| |
Db         64 GGGTGTCCCGCTCCGCCACCATCGTCATCGCTTACTTGATGAAGCACACTCGGATGACCA 123

Qy       1197 TAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATT 1256
              |   ||| ||||| | |||||| ||||  ||| |||| | ||| || |||||| | || |
Db        124 TGACTGATGCTTATAAATTTGTCAAAGGCAAACGACCAATTATCTCCCCAAACCTTAACT 183

Qy       1257 TTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAAC 1297
              |  |||| ||  | || || |  ||| |  |  | || |||
Db        184 TCATGGGGCAGTTGCTAGAGTTCGAGGAAGACCTAAACAAC 224


RESULT 12
US-09-016-434-1135
; Sequence 1135, Application US/09016434
; Patent No. 6500938
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1135:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2109 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g1418933
US-09-016-434-1135

  Query Match             2.7%;  Score 90.2;  DB 4;  Length 2109;
  Best Local Similarity   57.1%;  Pred. No. 5.6e-17;
  Matches  164;  Conservative    0;  Mismatches  123;  Indels    0;  Gaps    0;

Qy       1004 GAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCGTGG 1063
              |||| | | | |  ||   | ||  |   ||  ||  |  | ||  | |  | ||
Db       1105 GAGTTTAAATACAAGCAAATCCCCATCTCGGATCACTGGAGCCAAAACCTGTCCCAGTTT 1164

Qy       1064 TTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTAGTG 1123
              ||      | |  |   |||||| ||  ||||    | |   ||  |  |||| | ||
Db       1165 TTCCCTGAGGCCATTTCTTTCATAGATGAAGCCCGGGGCAAGAACTGTGGTGTCTTGGTA 1224

Qy       1124 CACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGG 1183
              || || || ||||| ||   |||||| | |||  |  || | || ||| | ||| ||| |
Db       1225 CATTGCTTGGCTGGCATTAGCCGCTCAGTCACTGTGACTGTGGCTTACCTTATGCAGAAG 1284

Qy       1184 ATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATATCT 1243
              | |  ||||  |  | || || ||     |||| |||   |||| | | |  |||||
Db       1285 CTCAATCTGTCGATGAACGATGCCTATGACATTGTCAAAATGAAAAAATCCAACATATCC 1344

Qy       1244 CCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGAT 1290
              || ||||||| ||  |||| || || |||||||  |||| || | |
Db       1345 CCTAACTTCAACTTCATGGGTCAGCTGCTGGACTTCGAGAGGACGCT 1391


RESULT 13
US-09-023-655-946
; Sequence 946, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 946:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2109 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1418933
US-09-023-655-946

Query Match 2.7%; Score 90.2; DB 4; Length 2109;
Best Local Similarity 57.1%; Pred. No. 5.6e-17;
Matches 164; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

Qy 1004 GAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCGTGG 1063
Db 1105 GAGTTTAAATACAAGCAAATCCCCATCTCGGATCACTGGAGCCAAAACCTGTCCCAGTTT 1164

Qy 1064 TTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTAGTG 1123
Db 1165 TTCCCTGAGGCCATTTCTTTCATAGATGAAGCCCGGGGCAAGAACTGTGGTGTCTTGGTA 1224

Qy 1124 CACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGG 1183
Db 1225 CATTGCTTGGCTGGCATTAGCCGCTCAGTCACTGTGACTGTGGCTTACCTTATGCAGAAG 1284

Qy 1184 ATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATATCT 1243
Db 1285 CTCAATCTGTCGATGAACGATGCCTATGACATTGTCAAAATGAAAAAATCCAACATATCC 1344

Qy 1244 CCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGAT 1290
Db 1345 CCTAACTTCAACTTCATGGGTCAGCTGCTGGACTTCGAGAGGACGCT 1391

RESULT 14
US-09-949-016-2615
; Sequence 2615, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2615
; LENGTH: 2475
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2615

Query Match 2.7%; Score 90.2; DB 4; Length 2475;
Best Local Similarity 57.1%; Pred. No. 6.4e-17;
Matches 164; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

Qy 1004 GAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCGTGG 1063
Db 1194 GAGTTTAAATACAAGCAAATCCCCATCTCGGATCACTGGAGCCAAAACCTGTCCCAGTTT 1253

Qy 1064 TTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTAGTG 1123
Db 1254 TTCCCTGAGGCCATTTCTTTCATAGATGAAGCCCGGGGCAAGAACTGTGGTGTCTTGGTA 1313

Qy 1124 CACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGG 1183
Db 1314 CATTGCTTGGCTGGCATTAGCCGCTCAGTCACTGTGACTGTGGCTTACCTTATGCAGAAG 1373

Qy 1184 ATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATATCT 1243
Db 1374 CTCAATCTGTCGATGAACGATGCCTATGACATTGTCAAAATGAAAAAATCCAACATATCC 1433

Qy 1244 CCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGAT 1290
Db 1434 CCTAACTTCAACTTCATGGGTCAGCTGCTGGACTTCGAGAGGACGCT 1480

RESULT 15
US-09-949-016-14992
; Sequence 14992, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14992
; LENGTH: 13782
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14992

Query Match 2.7%; Score 89.2; DB 4; Length 13782;
Best Local Similarity 69.5%; Pred. No. 5.1e-16;
Matches 121; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 915 TCACCTGCTTGCAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCA 974
Db 9650 TCCCGCCCCTCCAGGATCTGATGACGCAAAATGGAATAAGCTACGTCCTCAACGCCAGCA 9709

Qy 975 ATACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATG 1034
Db 9710 ACTCCTGCCCCAAGCCTGACTTCATCTGCGAGAGCCGCTTCATGCGGGTCCCCATCAACG 9769

Qy 1035 ACAGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTG 1088
Db 9770 ACAACTACTGTGAAAAACTGCTGCCCTGGCTGGACAAGTCCATCGAGTTCATCG 9823

Search completed: September 1, 2005, 02:13:59
Job time : 598 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 31, 2005, 11:02:23 ; Search time 43 Seconds
(without alignments)
17.360 Million cell updates/sec

Title: US-09-964-277-16
Perfect score: 52
Sequence: 1 VHCLAGISRS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	52	100.0	155	4	US-09-955-732A-6	Sequence 6, Appli
3	52	100.0	156	4	US-09-955-732A-3	Sequence 3, Appli
4	52	100.0	156	4	US-09-955-732A-4	Sequence 4, Appli
5	52	100.0	168	4	US-09-544-716-13	Sequence 13, Appl
6	52	100.0	168	4	US-09-557-921-13	Sequence 13, Appl
7	52	100.0	168	4	US-09-564-357-16	Sequence 16, Appl
8	52	100.0	168	4	US-09-619-380-15	Sequence 15, Appl
9	52	100.0	170	4	US-09-544-716-12	Sequence 12, Appl
10	52	100.0	170	4	US-09-544-716-14	Sequence 14, Appl
11	52	100.0	170	4	US-09-557-921-12	Sequence 12, Appl
12	52	100.0	170	4	US-09-557-921-15	Sequence 15, Appl
13	52	100.0	170	4	US-09-564-357-15	Sequence 15, Appl
14	52	100.0	170	4	US-09-564-357-17	Sequence 17, Appl
15	52	100.0	170	4	US-09-619-380-14	Sequence 14, Appl
16	52	100.0	170	4	US-09-619-380-16	Sequence 16, Appl
17	52	100.0	491	4	US-09-949-016-8486	Sequence 8486, Ap
18	52	100.0	661	4	US-09-949-016-9121	Sequence 9121, Ap
19	52	100.0	665	4	US-09-816-494-2	Sequence 2, Appli
20	51	98.1	156	4	US-09-955-732A-5	Sequence 5, Appli
21	51	98.1	207	4	US-09-270-767-44103	Sequence 44103, A
22	51	98.1	421	4	US-09-949-016-10488	Sequence 10488, A
23	48	92.3	226	3	US-09-045-973-8	Sequence 8, Appli
24	46	88.5	11	4	US-09-744-072-32	Sequence 32, Appl
25	46	88.5	23	4	US-09-544-716-5	Sequence 5, Appli
26	46	88.5	23	4	US-09-564-357-6	Sequence 6, Appli
27	46	88.5	24	4	US-09-619-380-4	Sequence 4, Appli
28	46	88.5	24	4	US-09-955-732A-17	Sequence 17, Appl
29	46	88.5	45	2	US-08-530-290-21	Sequence 21, Appl
30	46	88.5	72	2	US-08-530-290-19	Sequence 19, Appl
31	46	88.5	87	4	US-09-371-671B-7	Sequence 7, Appli
32	46	88.5	87	4	US-09-371-671B-8	Sequence 8, Appli
33	46	88.5	117	1	US-07-988-273-4	Sequence 4, Appli
34	46	88.5	117	5	PCT-US93-12019-4	Sequence 4, Appli
35	46	88.5	154	4	US-09-955-732A-7	Sequence 7, Appli
36	46	88.5	154	4	US-09-955-732A-8	Sequence 8, Appli
37	46	88.5	154	4	US-09-955-732A-9	Sequence 9, Appli
38	46	88.5	168	4	US-09-544-716-15	Sequence 15, Appl
39	46	88.5	168	4	US-09-557-921-16	Sequence 16, Appl
40	46	88.5	168	4	US-09-564-357-18	Sequence 18, Appl
41	46	88.5	168	4	US-09-619-380-17	Sequence 17, Appl
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45	46	88.5	169	4	US-09-557-921-18	Sequence 18, Appl
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47	46	88.5	169	4	US-09-564-357-20	Sequence 20, Appl
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49	46	88.5	169	4	US-09-619-380-19	Sequence 19, Appl
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52	46	88.5	198	3	US-09-045-973-5	Sequence 5, Appli
53	46	88.5	198	4	US-09-311-021-10	Sequence 10, Appl
54	46	88.5	302	4	US-09-702-705-806	Sequence 806, App
55	46	88.5	302	4	US-09-736-457-806	Sequence 806, App
56	46	88.5	302	4	US-09-614-124B-806	Sequence 806, App
57	46	88.5	302	4	US-09-671-325-806	Sequence 806, App
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61	46	88.5	314	3	US-09-164-193-22	Sequence 22, Appl
62	46	88.5	314	4	US-09-221-448A-22	Sequence 22, Appl
63	46	88.5	314	4	US-09-371-671B-11	Sequence 11, Appl
64	46	88.5	367	2	US-08-530-290-24	Sequence 24, Appl
65	46	88.5	367	2	US-08-990-379-6	Sequence 6, Appli
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67	46	88.5	393	2	US-08-990-379-4	Sequence 4, Appli
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84	45	86.5	100	4	US-09-270-767-44366	Sequence 44366, A
85	45	86.5	100	4	US-09-270-767-59790	Sequence 59790, A
86	45	86.5	154	4	US-09-955-732A-10	Sequence 10, Appl
87	45	86.5	171	4	US-09-544-716-18	Sequence 18, Appl
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90	45	86.5	171	4	US-09-619-380-20	Sequence 20, Appl
91	45	86.5	172	4	US-09-704-139-5	Sequence 5, Appli
92	45	86.5	172	4	US-09-816-494-8	Sequence 8, Appli
93	45	86.5	210	4	US-09-949-016-10939	Sequence 10939, A
94	45	86.5	384	4	US-09-949-016-6494	Sequence 6494, Ap
95	45	86.5	397	2	US-08-990-379-8	Sequence 8, Appli
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97	44	84.6	16	4	US-09-557-921-3	Sequence 3, Appli
98	44	84.6	72	2	US-08-530-290-20	Sequence 20, Appl
99	44	84.6	170	4	US-09-557-921-14	Sequence 14, Appl
100	44	84.6	174	4	US-09-564-357-22	Sequence 22, Appl

ALIGNMENTS

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RESULT 1
US-09-371-671B-9
; Sequence 9, Application US/09371671B
; Patent No. 6548743
; GENERAL INFORMATION:
;  APPLICANT: Sheen, Jen
;  APPLICANT:  Chiu, Wan-Ling
;  TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A
;  TITLE OF INVENTION:  DUAL-SPECIFICITY MAPK PHOSPHATASE AND USES THEREOF
;  FILE REFERENCE: 00786/370002
;  CURRENT APPLICATION NUMBER: US/09/371,671B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: 60/155,934
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/095,938
;  PRIOR FILING DATE: 1998-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 87
;   TYPE: PRT
;   ORGANISM: Rat rattus
US-09-371-671B-9

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Qy          1 VHCLAGISRS 10
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Db         34 VHCLAGISRS 43


RESULT 2
US-09-955-732A-6
; Sequence 6, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.433
;  CURRENT APPLICATION NUMBER: US/09/955,732A
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 155
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-955-732A-6

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Qy          1 VHCLAGISRS 10
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Db         96 VHCLAGISRS 105


RESULT 3
US-09-955-732A-3
; Sequence 3, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.433
;  CURRENT APPLICATION NUMBER: US/09/955,732A
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 156
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-955-732A-3

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Qy          1 VHCLAGISRS 10
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Db         97 VHCLAGISRS 106


RESULT 4
US-09-955-732A-4
; Sequence 4, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.433
;  CURRENT APPLICATION NUMBER: US/09/955,732A
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 156
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-955-732A-4

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  Best Local Similarity   100.0%;  Pred. No. 0.018;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         97 VHCLAGISRS 106


RESULT 5
US-09-544-716-13
; Sequence 13, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-9 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.415
;  CURRENT APPLICATION NUMBER: US/09/544,716
;  CURRENT FILING DATE:  2000-04-10
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-544-716-13

  Query Match             100.0%;  Score 52;  DB 4;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
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Db        108 VHCLAGISRS 117


RESULT 6
US-09-557-921-13
; Sequence 13, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-10 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.416
;  CURRENT APPLICATION NUMBER: US/09/557,921
;  CURRENT FILING DATE:  2000-04-20
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-557-921-13

  Query Match             100.0%;  Score 52;  DB 4;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
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Db        108 VHCLAGISRS 117


RESULT 7
US-09-564-357-16
; Sequence 16, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.413
;  CURRENT APPLICATION NUMBER: US/09/564,357
;  CURRENT FILING DATE:  2000-04-24
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-564-357-16

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  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
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Db        108 VHCLAGISRS 117


RESULT 8
US-09-619-380-15
; Sequence 15, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.418
;  CURRENT APPLICATION NUMBER: US/09/619,380
;  CURRENT FILING DATE:  2000-07-19
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-619-380-15

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  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        108 VHCLAGISRS 117


RESULT 9
US-09-544-716-12
; Sequence 12, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-9 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.415
;  CURRENT APPLICATION NUMBER: US/09/544,716
;  CURRENT FILING DATE:  2000-04-10
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-544-716-12

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
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Db        110 VHCLAGISRS 119


RESULT 10
US-09-544-716-14
; Sequence 14, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-9 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.415
;  CURRENT APPLICATION NUMBER: US/09/544,716
;  CURRENT FILING DATE:  2000-04-10
;  NUMBER OF SEQ ID NOS:  20
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; SEQ ID NO 14
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-544-716-14

  Query Match             100.0%;  Score 52;  DB 4;  Length 170;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
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Db        110 VHCLAGISRS 119


RESULT 11
US-09-557-921-12
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; Sequence 12, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-10 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.416
;  CURRENT APPLICATION NUMBER: US/09/557,921
;  CURRENT FILING DATE:  2000-04-20
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-557-921-12

  Query Match             100.0%;  Score 52;  DB 4;  Length 170;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
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Db        110 VHCLAGISRS 119


RESULT 12
US-09-557-921-15
; Sequence 15, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-10 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.416
;  CURRENT APPLICATION NUMBER: US/09/557,921
;  CURRENT FILING DATE:  2000-04-20
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-557-921-15

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Qy          1 VHCLAGISRS 10
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Db        110 VHCLAGISRS 119


RESULT 13
US-09-564-357-15
; Sequence 15, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.413
;  CURRENT APPLICATION NUMBER: US/09/564,357
;  CURRENT FILING DATE:  2000-04-24
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-564-357-15

  Query Match             100.0%;  Score 52;  DB 4;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 14
US-09-564-357-17
; Sequence 17, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.413
;  CURRENT APPLICATION NUMBER: US/09/564,357
;  CURRENT FILING DATE:  2000-04-24
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-564-357-17

  Query Match             100.0%;  Score 52;  DB 4;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 15
US-09-619-380-14
; Sequence 14, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.418
;  CURRENT APPLICATION NUMBER: US/09/619,380
;  CURRENT FILING DATE:  2000-07-19
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-619-380-14

  Query Match             100.0%;  Score 52;  DB 4;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 16
US-09-619-380-16
; Sequence 16, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
```

```
;  FILE REFERENCE: 200125.418
;  CURRENT APPLICATION NUMBER: US/09/619,380
;  CURRENT FILING DATE:  2000-07-19
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-619-380-16

  Query Match             100.0%;  Score 52;  DB 4;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 17
US-09-949-016-8486
; Sequence 8486, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8486
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8486

  Query Match             100.0%;  Score 52;  DB 4;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 0.059;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        401 VHCLAGISRS 410


RESULT 18
US-09-949-016-9121
; Sequence 9121, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9121
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9121

  Query Match             100.0%;  Score 52;  DB 4;  Length 661;
  Best Local Similarity   100.0%;  Pred. No. 0.081;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        280 VHCLAGISRS 289


RESULT 19
US-09-816-494-2
; Sequence 2, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel A.
;  TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
;  TITLE OF INVENTION:  PHOSPHATASE MOLECULES AND USES THEREFOR
;  FILE REFERENCE: 10448-030002
;  CURRENT APPLICATION NUMBER: US/09/816,494
;  CURRENT FILING DATE:  2001-03-23
;  PRIOR APPLICATION NUMBER: US 60/191,858
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 665
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-816-494-2

  Query Match             100.0%;  Score 52;  DB 4;  Length 665;
  Best Local Similarity   100.0%;  Pred. No. 0.081;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        242 VHCLAGISRS 251


RESULT 20
US-09-955-732A-5
; Sequence 5, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.433
;  CURRENT APPLICATION NUMBER: US/09/955,732A
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 156
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-955-732A-5

  Query Match             98.1%;  Score 51;  DB 4;  Length 156;
  Best Local Similarity   90.0%;  Pred. No. 0.028;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||:|||
Db         97 VHCLAGVSRS 106
```

```
RESULT 21
US-09-270-767-44103
; Sequence 44103, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44103
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-44103

  Query Match             98.1%;  Score 51;  DB 4;  Length 207;
  Best Local Similarity   90.0%;  Pred. No. 0.037;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||:|||
Db         96 VHCLAGVSRS 105


RESULT 22
US-09-949-016-10488
; Sequence 10488, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10488
;   LENGTH: 421
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10488

  Query Match             98.1%;  Score 51;  DB 4;  Length 421;
  Best Local Similarity   90.0%;  Pred. No. 0.078;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||:|||
Db        325 VHCLAGVSRS 334


RESULT 23
US-09-045-973-8
; Sequence 8, Application US/09045973
; Patent No. 6165767
;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Yue, Henry
;    APPLICANT:  Corley, Neil C.
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Baughn, Mariah
;    TITLE OF INVENTION:  PROTEIN PHOSPHATASE RELATED MOLECULES
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/045,973
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0491 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  226 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1495338
US-09-045-973-8

  Query Match             92.3%;  Score 48;  DB 3;  Length 226;
  Best Local Similarity   80.0%;  Pred. No. 0.15;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              |||:||:|||
Db         96 VHCVAGVSRS 105


RESULT 24
US-09-744-072-32
; Sequence 32, Application US/09744072
; Patent No. 6825328
; GENERAL INFORMATION:
;  APPLICANT: SCHERER, STEPHEN W.
;  APPLICANT:  MINASSIAN, BERGE A.
;  APPLICANT:  ROULEAU, GUY
;  APPLICANT:  DALGADO-ESCUETA, ANTONIO
;  TITLE OF INVENTION: LAFORA'S DISEASE GENE
;  FILE REFERENCE: 086671/0113
;  CURRENT APPLICATION NUMBER: US/09/744,072
;  CURRENT FILING DATE:  1999-07-20
;  PRIOR APPLICATION NUMBER: 60/093,495
;  PRIOR FILING DATE: 1998-07-20
;  PRIOR APPLICATION NUMBER: 60/130,269
;  PRIOR FILING DATE: 1999-04-21
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-744-072-32

  Query Match             88.5%;  Score 46;  DB 4;  Length 11;
```

```
  Best Local Similarity   90.0%;  Pred. No. 0.015;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db          1 VHCQAGISRS 10


RESULT 25
US-09-544-716-5
; Sequence 5, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-9 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.415
;  CURRENT APPLICATION NUMBER: US/09/544,716
;  CURRENT FILING DATE:  2000-04-10
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-544-716-5

  Query Match             88.5%;  Score 46;  DB 4;  Length 23;
  Best Local Similarity   90.0%;  Pred. No. 0.033;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db          5 VHCQAGISRS 14


RESULT 26
US-09-564-357-6
; Sequence 6, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.413
;  CURRENT APPLICATION NUMBER: US/09/564,357
;  CURRENT FILING DATE:  2000-04-24
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-564-357-6

  Query Match             88.5%;  Score 46;  DB 4;  Length 23;
  Best Local Similarity   90.0%;  Pred. No. 0.033;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db          5 VHCQAGISRS 14


RESULT 27
US-09-619-380-4
; Sequence 4, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.418
;  CURRENT APPLICATION NUMBER: US/09/619,380
;  CURRENT FILING DATE:  2000-07-19
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 24
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-619-380-4

  Query Match             88.5%;  Score 46;  DB 4;  Length 24;
  Best Local Similarity   90.0%;  Pred. No. 0.035;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db          6 VHCQAGISRS 15


RESULT 28
US-09-955-732A-17
; Sequence 17, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.433
;  CURRENT APPLICATION NUMBER: US/09/955,732A
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 24
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Conserved homology region from eight DSPs having
;   OTHER INFORMATION: MAP-kinase phosphatase activity
US-09-955-732A-17

  Query Match             88.5%;  Score 46;  DB 4;  Length 24;
  Best Local Similarity   90.0%;  Pred. No. 0.035;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db          6 VHCQAGISRS 15


RESULT 29
US-08-530-290-21
; Sequence 21, Application US/08530290
; Patent No. 5958721
;  GENERAL INFORMATION:
;    APPLICANT:  Marshall, Christopher John
;    APPLICANT:  Ashworth, Alan
;    APPLICANT:  Hughes, David Anthony
;    TITLE OF INVENTION:  Methods for Screening of Substances for
;    TITLE OF INVENTION:  Therapeutic Activity and Yeast for Use Therein
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
```

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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/530,290
;      FILING DATE:  14-DEC-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/GB94/00694
;      FILING DATE:  31-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9402573.1
;      FILING DATE:  10-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9307250.2
;      FILING DATE:  07-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bastian, Kevin L.
;      REGISTRATION NUMBER:  34,774
;      REFERENCE/DOCKET NUMBER:  084611-000000US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-530-290-21

  Query Match             88.5%;  Score 46;  DB 2;  Length 45;
  Best Local Similarity   90.0%;  Pred. No. 0.068;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db         34 VHCQAGISRS 43


RESULT 30
US-08-530-290-19
; Sequence 19, Application US/08530290
; Patent No. 5958721
;  GENERAL INFORMATION:
;    APPLICANT:  Marshall, Christopher John
;    APPLICANT:  Ashworth, Alan
;    APPLICANT:  Hughes, David Anthony
;    TITLE OF INVENTION:  Methods for Screening of Substances for
;    TITLE OF INVENTION:  Therapeutic Activity and Yeast for Use Therein
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/530,290
;      FILING DATE:  14-DEC-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/GB94/00694
;      FILING DATE:  31-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9402573.1
;      FILING DATE:  10-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9307250.2
;      FILING DATE:  07-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bastian, Kevin L.
;      REGISTRATION NUMBER:  34,774
;      REFERENCE/DOCKET NUMBER:  084611-000000US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  72 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-530-290-19

  Query Match             88.5%;  Score 46;  DB 2;  Length 72;
  Best Local Similarity   90.0%;  Pred. No. 0.11;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db         26 VHCQAGISRS 35


RESULT 31
US-09-371-671B-7
; Sequence 7, Application US/09371671B
; Patent No. 6548743
; GENERAL INFORMATION:
;  APPLICANT: Sheen, Jen
;  APPLICANT:  Chiu, Wan-Ling
;  TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A
;  TITLE OF INVENTION:  DUAL-SPECIFICITY MAPK PHOSPHATASE AND USES THEREOF
;  FILE REFERENCE: 00786/370002
;  CURRENT APPLICATION NUMBER: US/09/371,671B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: 60/155,934
;  PRIOR FILING DATE: 1999-01-14
;  PRIOR APPLICATION NUMBER: 60/095,938
;  PRIOR FILING DATE: 1998-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 87
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-371-671B-7

  Query Match             88.5%;  Score 46;  DB 4;  Length 87;
  Best Local Similarity   90.0%;  Pred. No. 0.14;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db         34 VHCQAGISRS 43


RESULT 32
US-09-371-671B-8
; Sequence 8, Application US/09371671B
; Patent No. 6548743
; GENERAL INFORMATION:
;  APPLICANT: Sheen, Jen
;  APPLICANT:  Chiu, Wan-Ling
;  TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A
;  TITLE OF INVENTION:  DUAL-SPECIFICITY MAPK PHOSPHATASE AND USES THEREOF
;  FILE REFERENCE: 00786/370002
;  CURRENT APPLICATION NUMBER: US/09/371,671B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: 60/155,934
;  PRIOR FILING DATE: 1999-01-14
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;  PRIOR APPLICATION NUMBER: 60/095,938
;  PRIOR FILING DATE: 1998-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 87
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-371-671B-8

  Query Match             88.5%;  Score 46;  DB 4;  Length 87;
  Best Local Similarity   90.0%;  Pred. No. 0.14;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db         34 VHCQAGISRS 43


RESULT 33
US-07-988-273-4
; Sequence 4, Application US/07988273
; Patent No. 5512434
;  GENERAL INFORMATION:
;    APPLICANT:  AARONSON, Stuart A.
;    APPLICANT:  BOTTARO, Donald P.
;    APPLICANT:  ISHIBASHI, Toshio
;    APPLICANT:  MIKI, Toru
;    TITLE OF INVENTION:  EXPRESSION CLONING OF A HUMAN
;    TITLE OF INVENTION:  PHOSPHATASE
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/988,273
;      FILING DATE:  19921214
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  40399/182 NIHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-988-273-4

  Query Match             88.5%;  Score 46;  DB 1;  Length 117;
  Best Local Similarity   90.0%;  Pred. No. 0.18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db         63 VHCQAGISRS 72


RESULT 34
PCT-US93-12019-4
; Sequence 4, Application PC/TUS9312019
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  EXPRESSION CLONING OF A HUMAN
;    TITLE OF INVENTION:  PHOSPHATASE
;    NUMBER OF SEQUENCES:  7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/12019
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,273
;      FILING DATE:  14-DEC-1992
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
PCT-US93-12019-4

  Query Match             88.5%;  Score 46;  DB 5;  Length 117;
  Best Local Similarity   90.0%;  Pred. No. 0.18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db         63 VHCQAGISRS 72


RESULT 35
US-09-955-732A-7
; Sequence 7, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.433
;  CURRENT APPLICATION NUMBER: US/09/955,732A
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 154
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-955-732A-7

  Query Match             88.5%;  Score 46;  DB 4;  Length 154;
  Best Local Similarity   90.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db         95 VHCQAGISRS 104


RESULT 36
US-09-955-732A-8
; Sequence 8, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.433
;  CURRENT APPLICATION NUMBER: US/09/955,732A
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 8
;   LENGTH: 154
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-955-732A-8

  Query Match             88.5%;  Score 46;  DB 4;  Length 154;
  Best Local Similarity   90.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db         95 VHCQAGISRS 104


RESULT 37
US-09-955-732A-9
; Sequence 9, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.433
;  CURRENT APPLICATION NUMBER: US/09/955,732A
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 154
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-955-732A-9

  Query Match             88.5%;  Score 46;  DB 4;  Length 154;
  Best Local Similarity   90.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db         95 VHCQAGISRS 104


RESULT 38
US-09-544-716-15
; Sequence 15, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-9 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.415
;  CURRENT APPLICATION NUMBER: US/09/544,716
;  CURRENT FILING DATE:  2000-04-10
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-544-716-15

  Query Match             88.5%;  Score 46;  DB 4;  Length 168;
  Best Local Similarity   90.0%;  Pred. No. 0.27;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db        109 VHCQAGISRS 118


RESULT 39
US-09-557-921-16
; Sequence 16, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-10 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.416
;  CURRENT APPLICATION NUMBER: US/09/557,921
;  CURRENT FILING DATE:  2000-04-20
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-557-921-16

  Query Match             88.5%;  Score 46;  DB 4;  Length 168;
  Best Local Similarity   90.0%;  Pred. No. 0.27;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db        109 VHCQAGISRS 118


RESULT 40
US-09-564-357-18
; Sequence 18, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.413
;  CURRENT APPLICATION NUMBER: US/09/564,357
;  CURRENT FILING DATE:  2000-04-24
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-564-357-18

  Query Match             88.5%;  Score 46;  DB 4;  Length 168;
  Best Local Similarity   90.0%;  Pred. No. 0.27;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db        109 VHCQAGISRS 118


RESULT 41
US-09-619-380-17
; Sequence 17, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.418
;  CURRENT APPLICATION NUMBER: US/09/619,380
;  CURRENT FILING DATE:  2000-07-19
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-619-380-17
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  Query Match             88.5%;  Score 46;  DB 4;  Length 168;
  Best Local Similarity   90.0%;  Pred. No. 0.27;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db        109 VHCQAGISRS 118


RESULT 42
US-09-544-716-16
; Sequence 16, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-9 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.415
;  CURRENT APPLICATION NUMBER: US/09/544,716
;  CURRENT FILING DATE:  2000-04-10
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-544-716-16

  Query Match             88.5%;  Score 46;  DB 4;  Length 169;
  Best Local Similarity   90.0%;  Pred. No. 0.27;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db        109 VHCQAGISRS 118


RESULT 43
US-09-544-716-17
; Sequence 17, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-9 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.415
;  CURRENT APPLICATION NUMBER: US/09/544,716
;  CURRENT FILING DATE:  2000-04-10
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-544-716-17

  Query Match             88.5%;  Score 46;  DB 4;  Length 169;
  Best Local Similarity   90.0%;  Pred. No. 0.27;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db        109 VHCQAGISRS 118


RESULT 44
US-09-557-921-17
; Sequence 17, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-10 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.416
;  CURRENT APPLICATION NUMBER: US/09/557,921
;  CURRENT FILING DATE:  2000-04-20
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-557-921-17

  Query Match             88.5%;  Score 46;  DB 4;  Length 169;
  Best Local Similarity   90.0%;  Pred. No. 0.27;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db        109 VHCQAGISRS 118


RESULT 45
US-09-557-921-18
; Sequence 18, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-10 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE:  200125.416
;  CURRENT APPLICATION NUMBER: US/09/557,921
;  CURRENT FILING DATE:  2000-04-20
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-557-921-18

  Query Match             88.5%;  Score 46;  DB 4;  Length 169;
  Best Local Similarity   90.0%;  Pred. No. 0.27;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||| ||||||
Db        109 VHCQAGISRS 118


Search completed: August 31, 2005, 11:11:30
Job time : 45 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 1, 2005, 02:14:01 ; Search time 379 Seconds
(without alignments)
2232.071 Million cell updates/sec

Title: US-09-964-277-21
Perfect score: 2668
Sequence: 1 MLPLSLQTVFSLYFWVNWRR.....LGKVGSQSSFSGSMEIIEVS 517

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool/US09964277/runat_31082005_120238_8492/app_query.fasta_1.711
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09964277_@CGN_1_1_69_@runat_31082005_120238_8492 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2606	97.7	1998	4	US-09-816-494-3	Sequence 3, Appli
2	2606	97.7	3544	4	US-09-816-494-1	Sequence 1, Appli
3	844	31.6	2377	4	US-09-920-668-3	Sequence 3, Appli
4	842	31.6	2351	4	US-09-949-016-3250	Sequence 3250, Ap
5	741.5	27.8	13782	4	US-09-949-016-14992	Sequence 14992, A
6	308	11.5	2283	4	US-09-949-016-4617	Sequence 4617, Ap
7	308	11.5	2303	4	US-09-922-146-3	Sequence 3, Appli
8	289.5	10.9	1238	4	US-09-702-705-803	Sequence 803, App
9	289.5	10.9	1238	4	US-09-736-457-803	Sequence 803, App
10	289.5	10.9	1238	4	US-09-614-124B-803	Sequence 803, App
11	289.5	10.9	1238	4	US-09-671-325-803	Sequence 803, App
12	289.5	10.9	1238	4	US-09-589-184-803	Sequence 803, App
13	289.5	10.9	1238	4	US-09-658-824-803	Sequence 803, App
14	287	10.8	1619	4	US-09-702-705-801	Sequence 801, App
15	287	10.8	1619	4	US-09-736-457-801	Sequence 801, App
16	287	10.8	1619	4	US-09-614-124B-801	Sequence 801, App
17	287	10.8	1619	4	US-09-671-325-801	Sequence 801, App
18	287	10.8	1619	4	US-09-589-184-801	Sequence 801, App
19	287	10.8	1619	4	US-09-658-824-801	Sequence 801, App
20	287	10.8	2064	4	US-09-702-705-825	Sequence 825, App
21	287	10.8	2064	4	US-09-736-457-825	Sequence 825, App
22	287	10.8	2064	4	US-09-614-124B-825	Sequence 825, App
23	287	10.8	2064	4	US-09-671-325-825	Sequence 825, App
24	287	10.8	2064	4	US-09-589-184-825	Sequence 825, App
25	287	10.8	2064	4	US-09-658-824-825	Sequence 825, App
26	287	10.8	2109	4	US-09-016-434-1135	Sequence 1135, Ap
27	287	10.8	2109	4	US-09-702-705-826	Sequence 826, App
28	287	10.8	2109	4	US-09-736-457-826	Sequence 826, App
29	287	10.8	2109	4	US-09-023-655-946	Sequence 946, App
30	287	10.8	2109	4	US-09-614-124B-826	Sequence 826, App
31	287	10.8	2109	4	US-09-671-325-826	Sequence 826, App
32	287	10.8	2109	4	US-09-589-184-826	Sequence 826, App
33	287	10.8	2109	4	US-09-658-824-826	Sequence 826, App
34	287	10.8	2240	4	US-09-016-434-1100	Sequence 1100, Ap
35	287	10.8	2363	4	US-09-949-016-2210	Sequence 2210, Ap
36	287	10.8	2475	4	US-09-949-016-2615	Sequence 2615, Ap
37	287	10.8	4637	4	US-09-702-705-804	Sequence 804, App
38	287	10.8	4637	4	US-09-736-457-804	Sequence 804, App
39	287	10.8	4637	4	US-09-614-124B-804	Sequence 804, App
40	287	10.8	4637	4	US-09-671-325-804	Sequence 804, App
41	287	10.8	4637	4	US-09-589-184-804	Sequence 804, App
42	287	10.8	4637	4	US-09-658-824-804	Sequence 804, App
43	286	10.7	2000	4	US-09-016-434-1291	Sequence 1291, Ap
44	286	10.7	2000	4	US-09-919-497-10	Sequence 10, Appl
45	286	10.7	2015	4	US-09-949-016-4969	Sequence 4969, Ap

ALIGNMENTS

RESULT 1
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494-3

Alignment Scores:

Pred. No.:	7.16e-257	Length:	1998
Score:	2606.00	Matches:	516
Percent Similarity:	90.21%	Conservative:	0
Best Local Similarity:	90.21%	Mismatches:	1
Query Match:	97.68%	Indels:	56
DB:	4	Gaps:	1

US-09-964-277-21 (1-517) x US-09-816-494-3 (1-1998)

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Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
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Db        281 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 340

Qy         21 AlaSerThrLeuPheThrCysLeuGln---------------------------------- 29
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Db        341 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 399

Qy         29 ------------------------------------------------------------ 29

Db        400 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 459

Qy         29 ------------------------------------------------------------ 29

Db        460 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 519

Qy         30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 579

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 639

Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 699

Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 759

Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 819

Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 879

Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 939

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 999

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1059

Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1119

Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1179

Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1180 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1239

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1299

Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1300 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1359

Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1360 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 1419

Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1420 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 1479

Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1480 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 1539

Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1540 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 1599

Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1600 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 1659

Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1660 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 1719

Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1720 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 1779

Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1780 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 1839

Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1840 CATGAAGAGAGCCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 1899

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1900 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 1959

Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
              |||||||||||||||||||||||||||||||||||
Db       1960 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 1995
```

RESULT 2
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2583)
US-09-816-494-1

Alignment Scores:

Pred. No.:	2e-256	Length:	3544
Score:	2606.00	Matches:	516
Percent Similarity:	90.21%	Conservative:	0
Best Local Similarity:	90.21%	Mismatches:	1
Query Match:	97.68%	Indels:	56
DB:	4	Gaps:	1

US-09-964-277-21 (1-517) x US-09-816-494-1 (1-3544)

```
Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
```

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Db        869 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 928
Qy         21 AlaSerThrLeuPheThrCysLeuGln-------------------------------- 29
Db        929 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 987
Qy         29 ------------------------------------------------------------ 29
Db        988 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 1047
Qy         29 ------------------------------------------------------------ 29
Db       1048 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 1107
Qy         30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
Db       1108 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 1167
Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
Db       1168 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 1227
Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
Db       1228 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 1287
Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db       1288 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1347
Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
Db       1348 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1407
Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
Db       1408 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1467
Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
Db       1468 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1527
Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
Db       1528 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1587
Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db       1588 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1647
Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
Db       1648 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1707
Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
Db       1708 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1767
Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
Db       1768 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1827
Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
Db       1828 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1887
Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
Db       1888 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1947
Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
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SEQ ID NO:15

SEQ ID NO:16

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Db       1948 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 2007
Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
Db       2008 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 2067
Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
Db       2068 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 2127
Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
Db       2128 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 2187
Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db       2188 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 2247
Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
Db       2248 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 2307
Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
Db       2308 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 2367
Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
Db       2368 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 2427
Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
Db       2428 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2487
Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
Db       2488 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2547
Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
Db       2548 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2583
```

RESULT 3
US-09-920-668-3
; Sequence 3, Application US/09920668
; Patent No. 6482644
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsert
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
; FILE REFERENCE: RTS-0246
; CURRENT APPLICATION NUMBER: US/09/920,668
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)...(2012)
US-09-920-668-3

Alignment Scores:

Pred. No.:	6.82e-76	Length:	2377
Score:	844.00	Matches:	216
Percent Similarity:	52.99%	Conservative:	59
Best Local Similarity:	41.62%	Mismatches:	142
Query Match:	31.63%	Indels:	102
DB:	4	Gaps:	19

US-09-964-277-21 (1-517) x US-09-920-668-3 (1-2377)

```
Qy         29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
Db        669 AAGGATCTGATGACGCAAAATGGAATAAGCTACGTCCTCAACGCCAGCAACTCCTGCCCC 728

Qy         49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
Db        729 AAGCCTGACTTCATCTGCGAGAGCCGCTTCATGCGGGTCCCCATCAACGACAACTACTGT 788

Qy         69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
Db        789 GAAAAACTGCTGCCCTGGCTGGACAAGTCCATCGAGTTCATCGATAAAGCCAAGCTCTCC 848

Qy         89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
Db        849 AGCTGCCAAGTCATCGTCCACTGTCTGGCTGGCATCTCCCGCTCTGCCACCATCGCCATC 908

Qy        109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128
Db        909 GCCTACATCATGAAGACCATGGGCATGTCCTCCGACGACGCCTACAGGTTCGTGAAGGAC 968

Qy        129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
Db        969 AGGCGCCCGTCCATCTCGCCCAACTTCAACTTCCTGGGCCAGCTGCTGGAGTACGAGCGC 1028

Qy        149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168
Db       1029 ACGCTGAAGCTGCTGGCCGCCCTGCAGGGCGACCCGGGC---------------------- 1067

Qy        169 GluLysProAsn---------GluProValProAlaValSerGluGlyGlyGlnLysSer 185
Db       1068 ---ACCCCCTCAGGGACGCCGGAGCCTCCGCCCAGTCCTGCCGCCGGGGGCCCCGCTGCCA 1124

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThr------SerGluAlaAlaGly 203
Db       1125 CGGCTGCCA------CCACCTACCTCAGAGAGCGCTGCCACAGGGAATGCGGCTGCCAGG 1178

Qy        204 GlnArgProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeu 223
Db       1179 GAGGGCGGCCTGAGCGCGGGCGGGGAGCCCCCCGCGCCCCCCACGCCCCCGGCG------ 1232

Qy        224 GluAspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGlu 243
Db       1233 ---ACCAGCGCACTGCAGCAGGGCCTGCGCGGCCTGCACCTCTCCTCGGACCGCCTGCAG 1289

Qy        244 AspSerAsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAla 263
Db       1290 GACACTAACCGCCTCAAGCGCTCCTTCTCCCTGGACATCAAGTCTGCC------------ 1337

Qy        264 SerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLys 283
Db       1338 ----------------------------------------------------TACGCC 1343

Qy        284 ProSerThrThrLeuAspGlyThrAsn----------------------LysLeuCys 295
Db       1344 CCTAGCAGGCGGCCCGACGGCCCCGGGCCCCCCGACCCCGGCGAGGCCCCGAAGCTCTGC 1403

Qy        296 GlnPhe---SerPro---------ValGlnGluLeuSerGluGlnThrProGluThrSer 311
Db       1404 AAGCTGGACAGCCCGTCGGGGGCCGCGCTGGGCCTGTCCTCGCCCAGCCCGGAC---AGC 1460

Qy        312 ProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSer 331
Db       1461 CCGGACGCCGCGCCTGAGGCGCGCCCACGGCCCCGCCGGCGGCCCCGGCCC--------- 1511

Qy        332 GlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 351
Db       1512 --------------------------------CCCGCCGGCTCCCCCGCGCGC------ 1532

Qy        352 LeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPhe 371
Db       1533 ---TCCCCCGCGCACAGCCTCGGC------------------------CTGAACTTC 1562

Qy        372 Gly---------LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeu 388
Db       1563 GGCGATGCGGCCCGGCAGACTCCGCGGCACGGCCTCTCGGCCCTGTCGGCGCCCGGGCTG 1622

Qy        389 LysGly---------------------------TrpHisSerAspIleLeuAlaProGln 399
Db       1623 CCCGGCCCTGGCCAGCCGGCCGGCCCCGGGGCCTGGGCACCGCCGCTTGACTCCCCA--- 1679

Qy        400 ThrSerThrProSerLeuThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyr 419
Db       1680 ---GGCACGCCGTCGCCCGACGGGCCCTGGTGCTTCAGCCCCGAG-------------- 1721

Qy        420 SerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeu 439
Db       1722 ------GGCGCACAGGGGGCGGGCGGGGTGCTGTTTGCGCCCTTCGGCCGGGCGGGCGCC 1775

Qy        440 ProThrCysGlyAspGlnValTyrSerValArgArgArgGlnLysProSerAspArgAla 459
Db       1776 CCGGGACCAGGCGGCGGCAGCGACCTGCGGCGGCGGGAGGCAGCGAGGGCTGAGCCCCGG 1835

Qy        460 AspSerArgArgSerTrpHisGluGluSerProPheGluLysGlnPheLysArgArgSer 479
Db       1836 GACGCGCGGACCGGCTGGCCCGAGGAGCCGGCCCCGGAGACGCAGTTCAAGCGCCGCAGC 1895

Qy        480 CysGlnMetGluPheGlyGluSerIleMetSerGluAsnArgSerArg---GluGluLeu 498
Db       1896 TGCCAGATGGAGTTCGAGGAGGGC---ATGGTGGAGGGGCGCGCGCGCGGCGAGGAGCTG 1952

Qy        499 GlyLysValGlySerGlnSerSerPheSerGlySerMetGluIleIleGluValSer 517
Db       1953 GCCGCCCTGGGCAAGCAGGCGAGCTTCTCGGGCAGCGTGGAGGTCATCGAGGTGTCC 2009
```

RESULT 4
US-09-949-016-3250
; Sequence 3250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3250
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3250

Alignment Scores:

Pred. No.:	1.07e-75	Length:	2351
Score:	842.00	Matches:	216
Percent Similarity:	52.79%	Conservative:	58
Best Local Similarity:	41.62%	Mismatches:	143
Query Match:	31.56%	Indels:	102
DB:	4	Gaps:	19

US-09-964-277-21 (1-517) x US-09-949-016-3250 (1-2351)

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Qy         29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
Db        643 AAGGATCTGATGACGCAAAATGGAATAAGCTACGTCCTCAACGCCAGCAACTCCTGCCCC 702

Qy         49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
Db        703 AAGCCTGACTTCATCTGCGAGAGCCGCTTCATGCGGGTCCCCATCAACGACAACTACTGT 762
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Qy        69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
Db       763 GAAAAACTGCTGCCCTGGCTGGACAAGTCCATCGAGTTCATCGATAAAGCCAAGCTCTCC 822

Qy        89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
Db       823 AGCTGCCAAGTCATCGTCCACTGTCTGGCTGGCATCTCCCGCTCTGCCACCATCGCCATC 882

Qy       109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128
Db       883 GCCTACATCATGAAGACCATGGGCATGTCCTCCGACGACGCCTACAGGTTCGTGAAGGAC 942

Qy       129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
Db       943 AGGCGCCCGTCCATCTCGCCCAACTTCAACTTCCTGGGCCAGCTGCTGGAGTACGAGCGC 1002

Qy       149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168
Db      1003 AGCCTGAAGCTGCTGGCCGCCCTGCAGGGCGACCCGGGC---------------------- 1041

Qy       169 GluLysProAsn---------GluProValProAlaValSerGluGlyGlyGlnLysSer 185
Db      1042 ---ACCCCCTCAGGGACGCCGGAGCCTCCGCCCAGTCCTGCCGCCGGGGCCCCGCTGCCA 1098

Qy       186 GluThrProLeuSerProProCysAlaAspSerAlaThr------SerGluAlaAlaGly 203
Db      1099 CGGCTGCCA------CCACCTACCTCAGAGAGCGCTGCCACAGGGAATGCGGCTGCCAGG 1152

Qy       204 GlnArgProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeu 223
Db      1153 GAGGGCGGCCTGAGCGCGGGCGGGGAGCCCCCCGCGCCCCCCACGCCCCCGGCG------ 1206

Qy       224 GluAspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGlu 243
Db      1207 ---ACCAGCGCACTGCAGCAGGGCCTGCGCGGCCTGCACCTCTCCTCCGGACCGCCTGCAG 1263

Qy       244 AspSerAsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAla 263
Db      1264 GACACTAACCGCCTCAAGCGCTCCTTCTCCCTGGACATCAAGTCTGCC------------ 1311

Qy       264 SerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLys 283
Db      1312 ------------------------------------------------------TACGCC 1317

Qy       284 ProSerThrThrLeuAspGlyThrAsn----------------------LysLeuCys 295
Db      1318 CCTAGCATGCGGCCCGACGGCCCCGGGCCCCCCGACCCCGGCGAGGCCCCGAAGCTCTGC 1377

Qy       296 GlnPhe---SerPro---------ValGlnGluLeuSerGluGlnThrProGluThrSer 311
Db      1378 AAGCTGGACAGCCCGTCGGGGGCCGCGCTGGGCCTGTCCTCGCCCATCCCGGAC---AGC 1434

Qy       312 ProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSer 331
Db      1435 CCGGACGCCGCGCCTGATGCGCGCCCACGGCCCCGCCGGCGGCCCCGGCCC--------- 1485

Qy       332 GlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 351
Db      1486 ------------------------------CCCGCCGGCTCCCCCGCGCGC------ 1506

Qy       352 LeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPhe 371
Db      1507 ---TCCCCCGCGCACAGCCTCGGC-------------------------CTGAACTTC 1536

Qy       372 Gly---------LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeu 388
Db      1537 GGCGATGCGGCCCGGCAGACTCCGCGGCACGGCCTCTCGGCCCTGTCGGCGCCCGGGCTG 1596

Qy       389 LysGly-------------------------TrpHisSerAspIleLeuAlaProGln 399
Db      1597 CCCGGCCCTGGCCAGCCGGCCGGCCCCGGGGCCTGGGCACCGCCGCTCGACTCCCCA--- 1653

Qy       400 ThrSerThrProSerLeuThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyr 419
Db      1654 ---GGCACGCCGTCGCCCGACGGGCCCTGGTGCTTCAGCCCCGAG---------------- 1695

Qy       420 SerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeu 439
Db      1696 ------GGCGCACAGGGGGCGGGCGGGGTGCTGTTTGCGCCCTTCGGCCGGGCGGGCGCC 1749

Qy       440 ProThrCysGlyAspGlnValTyrSerValArgArgArgGlnLysProSerAspArgAla 459
Db      1750 CCGGGACCAGGCGGCGGCAGCGACCTGCGGCGGCGGGAGGCAGCGAGGGCTGAGCCCCGG 1809

Qy       460 AspSerArgArgSerTrpHisGluGluSerProPheGluLysGlnPheLysArgArgSer 479
Db      1810 GACGCGCGGACCGGCTGGCCCGAGGAGCCGGCCCCGGAGACGCAGTTCAAGCGCCGCAGC 1869

Qy       480 CysGlnMetGluPheGlyGluSerIleMetSerGluAsnArgSerArg---GluGluLeu 498
Db      1870 TGCCAGATGGAGTTCGAGGAGGGC---ATGGTGGAGGGGCGCGCGCGCGGCGAGGAGCTG 1926

Qy       499 GlyLysValGlySerGlnSerSerPheSerGlySerMetGluIleIleGluValSer 517
Db      1927 GCCGCCCTGGGCAAGCAGGCGAGCTTCTCGGGCAGCGTGGAGGTCATCGAGGTGTCC 1983
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RESULT 5
US-09-949-016-14992
; Sequence 14992, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14992
; LENGTH: 13782
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14992

Alignment Scores:

Pred. No.:	5.29e-64	Length:	13782
Score:	741.50	Matches:	218
Percent Similarity:	41.64%	Conservative:	56
Best Local Similarity:	33.13%	Mismatches:	144
Query Match:	27.79%	Indels:	241
DB:	4	Gaps:	21

US-09-964-277-21 (1-517) x US-09-949-016-14992 (1-13782)

```
Qy        28 LeuGlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCys 47
Db      9658 CTCCAGGATCTGATGACGCAAAATGGAATAAGCTACGTCCTCAACGCCAGCAACTCCTGC 9717

Qy        48 ProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPhe 67
Db      9718 CCCAAGCCTGACTTCATCTGCGAGAGCCGCTTCATGCGGGTCCCCATCAACGACAACTAC 9777

Qy        68 CysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGlu------------ 83
Db      9778 TGTGAAAAACTGCTGCCCTGGCTGGACAAGTCCATCGAGTTCATCGG-TGAGTCTGCGGT 9836

Qy        83 ------------------------------------------------------------ 83
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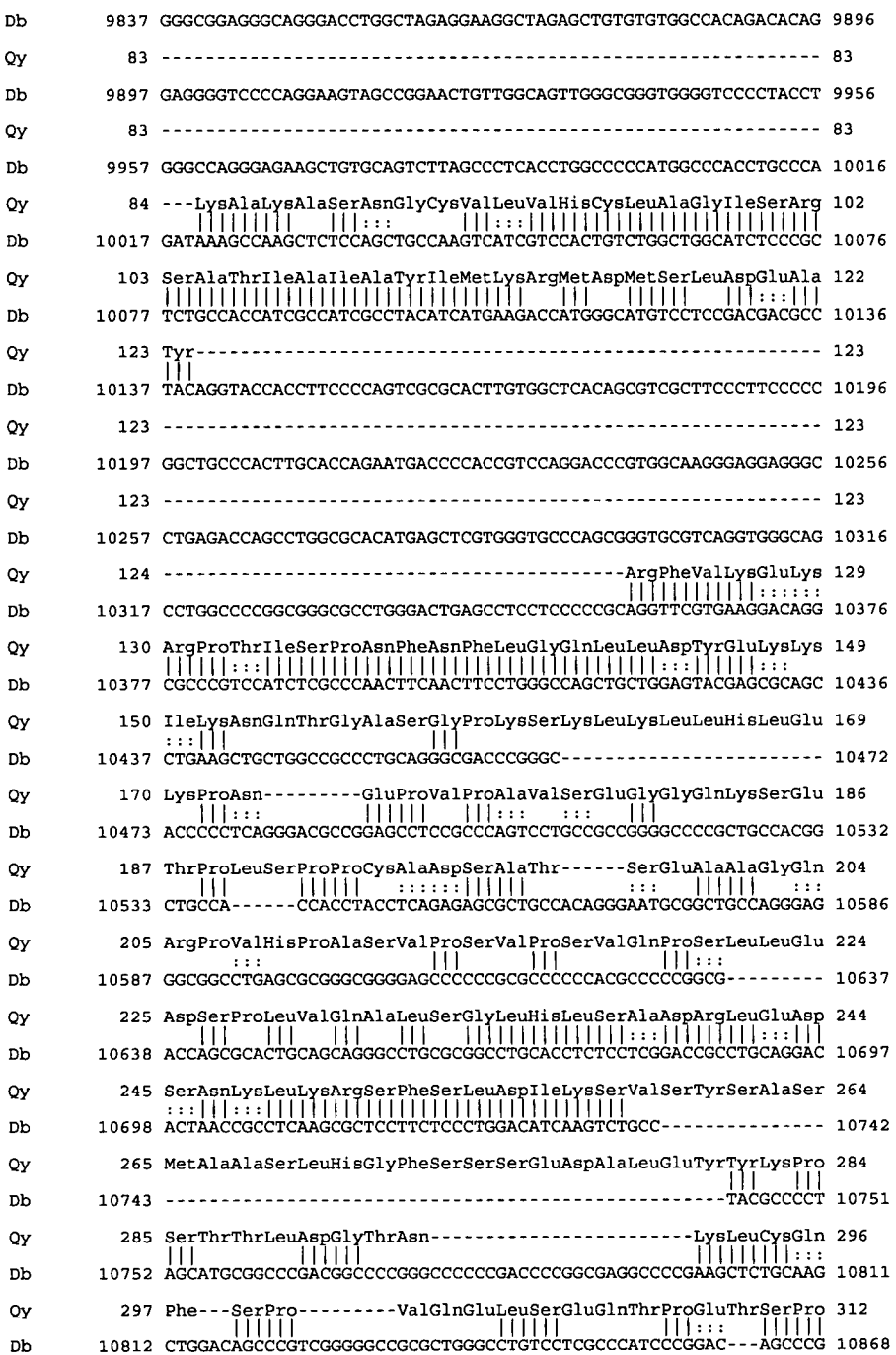

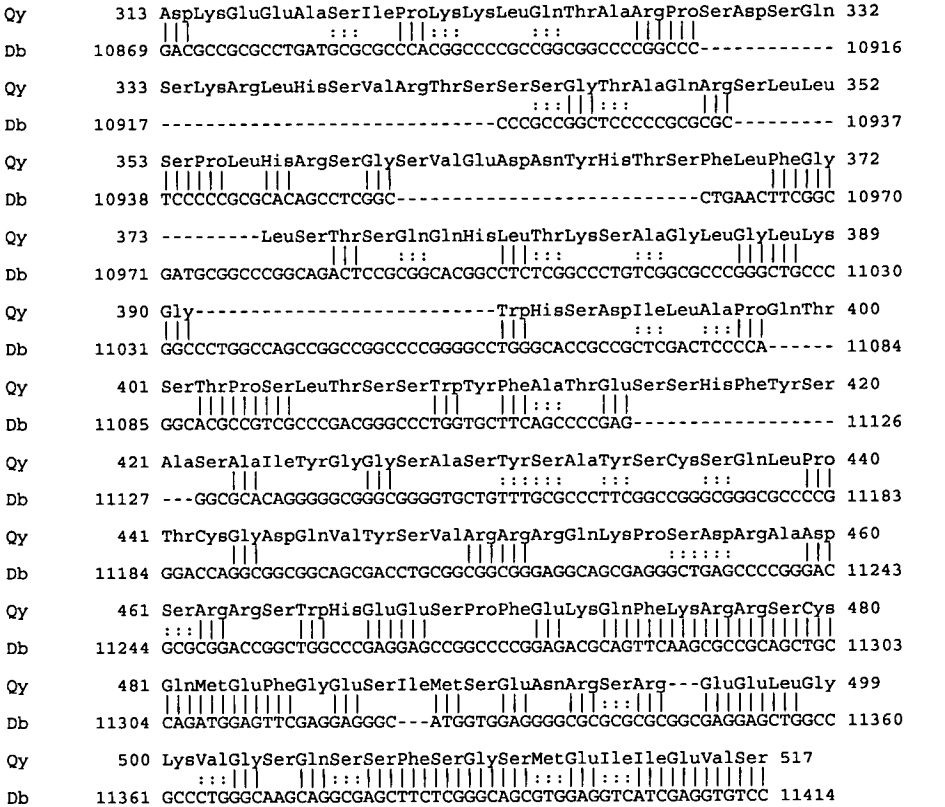

RESULT 6
US-09-949-016-4617
; Sequence 4617, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4617
; LENGTH: 2283
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4617

Alignment Scores:
Pred. No.: 6.54e-21 Length: 2283
Score: 308.00 Matches: 74

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Percent Similarity:     51.95%          Conservative:  46
Best Local Similarity:  32.03%          Mismatches:    77
Query Match:            11.54%          Indels:        34
DB:                     4               Gaps:          6

US-09-964-277-21 (1-517) x US-09-949-016-4617 (1-2283)

Qy           3 ProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArgAlaSer 22
Db         699 CCAGTGGGGCTGCGGGCATCCTTCCCTGTCCAGATCCTGCCCAACCTCTATCTGGGCAGT 758

Qy          23 ThrLeuPheThrCysLeuGlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsn 42
Db         759 GCCCGGGATTCCGCCAATTTGGAGAGCCTGGCCAAACTGGGCATCCGCTACATCCTCAAT 818

Qy          43 AlaSerAsnThrCysPro--------------LysProAspPheIleProGluSerHis 57
Db         819 GTCACCCCCAACCTCCCAAACTTCTTCGAGAAGAATGGTGACTTT------------CAC 866

Qy          58 PheLeuArgValProValAsnAspSerPheCysGluLysIleLeuProTrpLeuAspLys 77
Db         867 TACAAGCAGATCCCCATCTCCGACCACTGGAGCCAGAACCTGTCGCGGTTCTTTCCGGAG 926

Qy          78 SerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysValLeuValHisCysLeu 97
Db         927 GCCATTGAGTTCATTGATGAGGCCTTGTCCCAGAACTGCGGGGTGCTCGTCCACTGCTTG 986

Qy          98 AlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMetLysArgMetAspMet 117
Db         987 GCGGGGGTCAGCCGTTCTGTCACCGTCACTGTGGCCTACCTCATGCAGAAGCTCCACCTC 1046

Qy         118 SerLeuAspGluAlaTyrArgPheValLysGluLysArgProThrIleSerProAsnPhe 137
Db        1047 TCTCTCAACGATGCCTATGACCTGGTCAAGAGGAAGAAGTCTAACATCTCCCCCAACTTC 1106

Qy         138 AsnPheLeuGlyGlnLeuLeuAspTyrGluLysLysIleLysAsnGlnThrGlyAlaSer 157
Db        1107 AACTTCATGGGGCAGTTGCTGGACTTTGAGCGCAGCTTG---------------------- 1145

Qy         158 GlyProLysSerLysLeuLysLeuLeuHisLeuGluLysProAsnGluProValProAla 177
Db        1146 ------------CGGCTGGAGGAGCGCCACTCGCAGGAGCAG------------------ 1175

Qy         178 ValSerGluGlyGlyGlnLysSerGluThrProLeuSerPro---------------Pro 192
Db        1176 ---GGCAGTGGGGGGCAGGCATCTGCGGCCTCCAACCCGCCCTCCTTCTTCACCACCCCC 1232

Qy         193 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProVal------HisProAla 210
Db        1233 ACCAGTGATGGCGCCTTCGAGCTGGCCCCCACCTAGGGCCCCGTGGCCGGCAGGCCGGCC 1292

Qy         211 SerValProSerValProSerValGlnProSer 221
Db        1293 CCTGCCCCACCCCCACCCACGGGTGTCCCTGCC 1325

RESULT 7
US-09-922-146-3
; Sequence 3, Application US/09922146
; Patent No. 6566133
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Brett P. Monia
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
;  FILE REFERENCE: RTS-0252
;  CURRENT APPLICATION NUMBER: US/09/922,146
;  CURRENT FILING DATE:  2001-08-01
;  NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
;   LENGTH: 2303
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (114)...(1268)
US-09-922-146-3

Alignment Scores:
Pred. No.:              6.64e-21        Length:        2303
Score:                  308.00          Matches:       74
Percent Similarity:     51.95%          Conservative:  46
Best Local Similarity:  32.03%          Mismatches:    77
Query Match:            11.54%          Indels:        34
DB:                     4               Gaps:          6

US-09-964-277-21 (1-517) x US-09-922-146-3 (1-2303)

Qy           3 ProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArgAlaSer 22
Db         699 CCAGTGGGGCTGCGGGCATCCTTCCCTGTCCAGATCCTGCCCAACCTCTATCTGGGCAGT 758

Qy          23 ThrLeuPheThrCysLeuGlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsn 42
Db         759 GCCCGGGATTCCGCCAATTTGGAGAGCCTGGCCAAACTGGGCATCCGCTACATCCTCAAT 818

Qy          43 AlaSerAsnThrCysPro--------------LysProAspPheIleProGluSerHis 57
Db         819 GTCACCCCCAACCTCCCAAACTTCTTCGAGAAGAATGGTGACTTT------------CAC 866

Qy          58 PheLeuArgValProValAsnAspSerPheCysGluLysIleLeuProTrpLeuAspLys 77
Db         867 TACAAGCAGATCCCCATCTCCGACCACTGGAGCCAGAACCTGTCGCGGTTCTTTCCGGAG 926

Qy          78 SerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysValLeuValHisCysLeu 97
Db         927 GCCATTGAGTTCATTGATGAGGCCTTGTCCCAGAACTGCGGGGTGCTCGTCCACTGCTTG 986

Qy          98 AlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMetLysArgMetAspMet 117
Db         987 GCGGGGGTCAGCCGTTCTGTCACCGTCACTGTGGCCTACCTCATGCAGAAGCTCCACCTC 1046

Qy         118 SerLeuAspGluAlaTyrArgPheValLysGluLysArgProThrIleSerProAsnPhe 137
Db        1047 TCTCTCAACGATGCCTATGACCTGGTCAAGAGGAAGAAGTCTAACATCTCCCCCAACTTC 1106

Qy         138 AsnPheLeuGlyGlnLeuLeuAspTyrGluLysLysIleLysAsnGlnThrGlyAlaSer 157
Db        1107 AACTTCATGGGGCAGTTGCTGGACTTTGAGCGCAGCTTG---------------------- 1145

Qy         158 GlyProLysSerLysLeuLysLeuLeuHisLeuGluLysProAsnGluProValProAla 177
Db        1146 ------------CGGCTGGAGGAGCGCCACTCGCAGGAGCAG------------------ 1175

Qy         178 ValSerGluGlyGlyGlnLysSerGluThrProLeuSerPro---------------Pro 192
Db        1176 ---GGCAGTGGGGGGCAGGCATCTGCGGCCTCCAACCCGCCCTCCTTCTTCACCACCCCC 1232

Qy         193 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProVal------HisProAla 210
Db        1233 ACCAGTGATGGCGCCTTCGAGCTGGCCCCCACCTAGGGCCCCGTGGCCGGCAGGCCGGCC 1292

Qy         211 SerValProSerValProSerValGlnProSer 221
Db        1293 CCTGCCCCACCCCCACCCACGGGTGTCCCTGCC 1325

RESULT 8
US-09-702-705-803
; Sequence 803, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
```

```
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C14
;  CURRENT APPLICATION NUMBER: US/09/702,705
;  CURRENT FILING DATE:  2000-10-30
;  NUMBER OF SEQ ID NOS:  1833
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 803
;   LENGTH: 1238
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-702-705-803

Alignment Scores:
Pred. No.:              1.73e-19        Length:         1238
Score:                  289.50          Matches:        72
Percent Similarity:     54.15%          Conservative:   39
Best Local Similarity:  35.12%          Mismatches:     69
Query Match:            10.85%          Indels:         25
DB:                     4               Gaps:           6

US-09-964-277-21 (1-517) x US-09-702-705-803 (1-1238)

Qy         29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
              :::::::::::          ::::::      :::::::   ::::::   ::::::
Db        693 AGAGACATGCTGGACGCCCTGGGCATCACGGCTCTGTTGAATGTCTCCTCGGACTGCCCA 752

Qy         49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
                    |||                 :::      :::::::   |||:::
Db        753 AAC---CACTTTGAAGGACACTATCAGTACAAGTGCATCCCAGTGGAAGATAACCACAAG 809

Qy         69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
                  |||      |||       :::::::::::::::|||:::      |||
Db        810 GCCGACATCAGCTCCTGGTTCATGGAAGCCATAGAGTACATCGATGCCGTGAAGGACTGC 869

Qy         89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
                 |||  ||||||||||||||   ||||||||||||||||||||||||||||   :::
Db        870 CGTGGGCGCGTGCTGGTGCACTGCCAGGCGGGCATCTCGCGGTCGGCCACCATCTGCCTG 929

Qy        109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128
              ||||||:::|||   :::      :::   |||:::||||||:::   |||||||||:::
Db        930 GCCTACCTGATGATGAAGAAACGGGTGAGGCTGGAGGAGGCCTTCGAGTTCGTTAAGCAG 989

Qy        129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
              :::|||      |||||||||||||:::|||:::||||||||||||   :::|||
Db        990 CGCCGCAGCATCATCTCGCCCAACTTCAGCTTCATGGGGCAGCTGCTGCAGTTCGAGTCC 1049

Qy        149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168
              ::::::          :::   |||:::          |||
Db       1050 CAGGTGCTGGCCACGTCCTGTGCTGCGGAGGCTGCTAGC---------------------- 1088

Qy        169 GluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrPro 188
                 |||:::   |||:::                    |||::::::   :::||||||
Db       1089 ------CCCTCGGGACCCCTG-----------------GGGGAGCGGGGCAAGACCCCC 1124

Qy        189 LeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHis 208
                 :::|||                  ||||||:::                  ||||||
Db       1125 GCCACCCCC-----------------ACCTCGCAGTTCGTCTTCAGCTTTCCGGTC--- 1163

Qy        209 ProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeu 228
                    |||   |||   ||||||      |||   |||         ||||||:::
Db       1164 TCCGTGGGCGTGCACTCGGCCCCCAGCAGCCTGCCCTACCTG------CACAGCCCCATC 1217

Qy        229 ValGlnAlaLeuSer 233
                    :::   |||
Db       1218 ACCACCTCTCCCAGC 1232

RESULT 9
US-09-736-457-803
; Sequence 803, Application US/09736457
; Patent No. 6509448
```

```
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Wang, Aijun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C15
;  CURRENT APPLICATION NUMBER: US/09/736,457
;  CURRENT FILING DATE:  2000-12-13
;  NUMBER OF SEQ ID NOS:  1864
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 803
;   LENGTH: 1238
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-736-457-803

Alignment Scores:
Pred. No.:              1.73e-19        Length:         1238
Score:                  289.50          Matches:        72
Percent Similarity:     54.15%          Conservative:   39
Best Local Similarity:  35.12%          Mismatches:     69
Query Match:            10.85%          Indels:         25
DB:                     4               Gaps:           6

US-09-964-277-21 (1-517) x US-09-736-457-803 (1-1238)

Qy         29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
              :::::::::::          ::::::      :::::::   ::::::   ::::::
Db        693 AGAGACATGCTGGACGCCCTGGGCATCACGGCTCTGTTGAATGTCTCCTCGGACTGCCCA 752

Qy         49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
                    |||                 :::      :::|||||   |||:::
Db        753 AAC---CACTTTGAAGGACACTATCAGTACAAGTGCATCCCAGTGGAAGATAACCACAAG 809

Qy         69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
                  |||      |||       :::::::::::::::|||:::      |||
Db        810 GCCGACATCAGCTCCTGGTTCATGGAAGCCATAGAGTACATCGATGCCGTGAAGGACTGC 869

Qy         89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
                 |||  ||||||||||||||   ||||||||||||||||||||||||||||   :::
Db        870 CGTGGGCGCGTGCTGGTGCACTGCCAGGCGGGCATCTCGCGGTCGGCCACCATCTGCCTG 929

Qy        109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128
              ||||||:::|||   :::      :::   |||:::|||||:::   |||||||||:::
Db        930 GCCTACCTGATGATGAAGAAACGGGTGAGGCTGGAGGAGGCCTTCGAGTTCGTTAAGCAG 989

Qy        129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
              :::|||      |||||||||||||:::|||:::||||||||||||   :::|||
Db        990 CGCCGCAGCATCATCTCGCCCAACTTCAGCTTCATGGGGCAGCTGCTGCAGTTCGAGTCC 1049

Qy        149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168
              ::::::          :::   |||:::          |||
Db       1050 CAGGTGCTGGCCACGTCCTGTGCTGCGGAGGCTGCTAGC---------------------- 1088

Qy        169 GluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrPro 188
                 |||:::   |||:::                    |||::::::   :::||||||
Db       1089 ------CCCTCGGGACCCCTG-----------------GGGGAGCGGGGCAAGACCCCC 1124

Qy        189 LeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHis 208
                 :::|||                  ||||||:::                  ||||||
Db       1125 GCCACCCCC-----------------ACCTCGCAGTTCGTCTTCAGCTTTCCGGTC--- 1163

Qy        209 ProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeu 228
                    |||   |||   ||||||      |||   |||         ||||||:::
Db       1164 TCCGTGGGCGTGCACTCGGCCCCCAGCAGCCTGCCCTACCTG------CACAGCCCCATC 1217
```

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Qy        229 ValGlnAlaLeuSer 233
                  :::   |||
Db       1218 ACCACCTCTCCCAGC 1232
```

RESULT 10
US-09-614-124B-803
; Sequence 803, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 803
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-803

Alignment Scores:

Pred. No.:	1.73e-19	Length:	1238
Score:	289.50	Matches:	72
Percent Similarity:	54.15%	Conservative:	39
Best Local Similarity:	35.12%	Mismatches:	69
Query Match:	10.85%	Indels:	25
DB:	4	Gaps:	6

US-09-964-277-21 (1-517) x US-09-614-124B-803 (1-1238)

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Qy         29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
              :::::::::::::         |||||||      :::|||||||   |||:::   ||||||
Db        693 AGAGACATGCTGGACGCCCTGGGCATCACGGCTCTGTTGAATGTCTCCTCGGACTGCCCA 752

Qy         49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
                  |||                    :::      :::|||||||   |||:::
Db        753 AAC---CACTTTGAAGGACACTATCAGTACAAGTGCATCCCAGTGGAAGATAACCACAAG 809

Qy         69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
                 |||       |||       ::::::::::::::|||:::        |||
Db        810 GCCGACATCAGCTCCTGGTTCATGGAAGCCATAGAGTACATCGATGCCGTGAAGGACTGC 869

Qy         89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
                |||   |||||||||||||||   |||||||||||||||||||||||||||||   :::
Db        870 CGTGGGCGCGTGCTGGTGCACTGCCAGGCGGGCATCTCGCGGTCGGCCACCATCTGCCTG 929

Qy        109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128
              ||||||:::|||   :::       :::   |||:::|||||||:::   |||||||||:::
Db        930 GCCTACCTGATGATGAAGAAACGGGTGAGGCTGGAGGAGGCCTTCGAGTTCGTTAAGCAG 989

Qy        129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
              :::|||      |||||||||||||||:::|||:::|||||||||||||   :::|||
Db        990 CGCCGCAGCATCATCTCGCCCAACTTCAGCTTCATGGGGCAGCTGCTGCAGTTCGAGTCC 1049

Qy        149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168
              ::::::         :::   |||:::         |||
Db       1050 CAGGTGCTGGCCACGTCCTGTGCTGCGGAGGCTGCTAGC---------------------- 1088

Qy        169 GluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrPro 188
                 |||:::   |||:::                  |||::::::   :::||||||
Db       1089 ------CCCTCGGGACCCCTG-----------------GGGGAGCGGGGCAAGACCCCC 1124

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Qy        189 LeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHis 208
                 :::|||                  ||||||:::          ||||||
Db       1125 GCCACCCCC----------------ACCTCGCAGTTCGTCTTCAGCTTTCCGGTC--- 1163

Qy        209 ProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeu 228
                    |||   |||   ||||||     |||   |||         ||||||:::
Db       1164 TCCGTGGGCGTGCACTCGGCCCCCAGCAGCCTGCCCTACCTG------CACAGCCCCATC 1217

Qy        229 ValGlnAlaLeuSer 233
                  :::   |||
Db       1218 ACCACCTCTCCCAGC 1232
```

RESULT 11
US-09-671-325-803
; Sequence 803, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 803
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-803

Alignment Scores:

Pred. No.:	1.73e-19	Length:	1238
Score:	289.50	Matches:	72
Percent Similarity:	54.15%	Conservative:	39
Best Local Similarity:	35.12%	Mismatches:	69
Query Match:	10.85%	Indels:	25
DB:	4	Gaps:	6

US-09-964-277-21 (1-517) x US-09-671-325-803 (1-1238)

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Qy         29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
              :::::::::::::         |||||||      :::|||||||   |||:::   ||||||
Db        693 AGAGACATGCTGGACGCCCTGGGCATCACGGCTCTGTTGAATGTCTCCTCGGACTGCCCA 752

Qy         49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
                  |||                    :::      :::|||||||   |||:::
Db        753 AAC---CACTTTGAAGGACACTATCAGTACAAGTGCATCCCAGTGGAAGATAACCACAAG 809

Qy         69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
                 |||       |||       ::::::::::::::|||:::        |||
Db        810 GCCGACATCAGCTCCTGGTTCATGGAAGCCATAGAGTACATCGATGCCGTGAAGGACTGC 869

Qy         89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
                |||   |||||||||||||||   |||||||||||||||||||||||||||||   :::
Db        870 CGTGGGCGCGTGCTGGTGCACTGCCAGGCGGGCATCTCGCGGTCGGCCACCATCTGCCTG 929

Qy        109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128
              ||||||:::|||   :::       :::   |||:::|||||||:::   |||||||||:::
Db        930 GCCTACCTGATGATGAAGAAACGGGTGAGGCTGGAGGAGGCCTTCGAGTTCGTTAAGCAG 989

Qy        129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
              :::|||      |||||||||||||||:::|||:::|||||||||||||   :::|||
Db        990 CGCCGCAGCATCATCTCGCCCAACTTCAGCTTCATGGGGCAGCTGCTGCAGTTCGAGTCC 1049
```
```

```
Qy        149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168
              ::::::         :::   |||:::        |||
Db       1050 CAGGTGCTGGCCACGTCCTGTGCTGCGGAGGCTGCTAGC---------------------- 1088

Qy        169 GluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrPro 188
                 |||:::   |||:::                   |||::::::   :::||||||
Db       1089 ------CCCTCGGGACCCCTG-----------------GGGGAGCGGGGCAAGACCCCC 1124

Qy        189 LeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHis 208
                 :::|||                  ||||||:::                  ||||||
Db       1125 GCCACCCCC-----------------ACCTCGCAGTTCGTCTTCAGCTTTCCGGTC--- 1163

Qy        209 ProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeu 228
                    |||   |||   ||||||      |||   |||         ||||||:::
Db       1164 TCCGTGGGCGTGCACTCGGCCCCCAGCAGCCTGCCCTACCTG------CACAGCCCCATC 1217

Qy        229 ValGlnAlaLeuSer 233
                    :::   |||
Db       1218 ACCACCTCTCCCAGC 1232

RESULT 12
US-09-589-184-803
; Sequence 803, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C8
;  CURRENT APPLICATION NUMBER: US/09/589,184
;  CURRENT FILING DATE:  2000-06-05
;  NUMBER OF SEQ ID NOS:  827
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 803
;   LENGTH: 1238
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-589-184-803

Alignment Scores:
Pred. No.:              1.73e-19        Length:         1238
Score:                  289.50          Matches:        72
Percent Similarity:     54.15%          Conservative:   39
Best Local Similarity:  35.12%          Mismatches:     69
Query Match:            10.85%          Indels:         25
DB:                     4               Gaps:           6

US-09-964-277-21 (1-517) x US-09-589-184-803 (1-1238)

Qy         29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
              ::::::::::::        ||||||      :::||||||   |||:::   ||||||
Db        693 AGAGACATGCTGGACGCCCTGGGCATCACGGCTCTGTTGAATGTCTCCTCGGACTGCCCA 752

Qy         49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
                    |||                 :::      :::||||||   |||:::
Db        753 AAC---CACTTTGAAGGACACTATCAGTACAAGTGCATCCCAGTGGAAGATAACCACAAG 809

Qy         69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
                 |||       |||      :::::::::::::|||:::       |||
Db        810 GCCGACATCAGCTCCTGGTTCATGGAAGCCATAGAGTACATCGATGCCGTGAAGGACTGC 869

Qy         89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
              |||   ||||||||||||||   ||||||||||||||||||||||||||   :::
Db        870 CGTGGGCGCGTGCTGGTGCACTGCCAGGCGGGCATCTCGCGGTCGGCCACCATCTGCCTG 929

Qy        109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128
              ||||||:::|||   :::      :::   |||:::||||||:::   |||||||||:::
Db        930 GCCTACCTGATGATGAAGAAACGGGTGAGGCTGGAGGAGGCCTTCGAGTTCGTTAAGCAG 989

Qy        129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
              :::|||      ||||||||||||||:::|||:::||||||||||||   :::|||
Db        990 CGCCGCAGCATCATCTCGCCCAACTTCAGCTTCATGGGGCAGCTGCTGCAGTTCGAGTCC 1049

Qy        149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168
              ::::::         :::   |||:::        |||
Db       1050 CAGGTGCTGGCCACGTCCTGTGCTGCGGAGGCTGCTAGC---------------------- 1088

Qy        169 GluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrPro 188
                 |||:::   |||:::                   |||::::::   :::||||||
Db       1089 ------CCCTCGGGACCCCTG-----------------GGGGAGCGGGGCAAGACCCCC 1124

Qy        189 LeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHis 208
                 :::|||                  ||||||:::                  ||||||
Db       1125 GCCACCCCC-----------------ACCTCGCAGTTCGTCTTCAGCTTTCCGGTC--- 1163

Qy        209 ProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeu 228
                    |||   |||   ||||||      |||   |||         ||||||:::
Db       1164 TCCGTGGGCGTGCACTCGGCCCCCAGCAGCCTGCCCTACCTG------CACAGCCCCATC 1217

Qy        229 ValGlnAlaLeuSer 233
                    :::   |||
Db       1218 ACCACCTCTCCCAGC 1232

RESULT 13
US-09-658-824-803
; Sequence 803, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C11
;  CURRENT APPLICATION NUMBER: US/09/658,824
;  CURRENT FILING DATE:  2000-09-08
;  NUMBER OF SEQ ID NOS:  1788
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 803
;   LENGTH: 1238
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-658-824-803

Alignment Scores:
Pred. No.:              1.73e-19        Length:         1238
Score:                  289.50          Matches:        72
Percent Similarity:     54.15%          Conservative:   39
Best Local Similarity:  35.12%          Mismatches:     69
Query Match:            10.85%          Indels:         25
DB:                     4               Gaps:           6

US-09-964-277-21 (1-517) x US-09-658-824-803 (1-1238)

Qy         29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
              ::::::::::::        ||||||      :::||||||   |||:::   ||||||
Db        693 AGAGACATGCTGGACGCCCTGGGCATCACGGCTCTGTTGAATGTCTCCTCGGACTGCCCA 752

Qy         49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
                    |||                 :::      :::||||||   |||:::
Db        753 AAC---CACTTTGAAGGACACTATCAGTACAAGTGCATCCCAGTGGAAGATAACCACAAG 809

Qy         69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
```

```
Db        810 GCCGACATCAGCTCCTGGTTCATGGAAGCCATAGAGTACATCGATGCCGTGAAGGACTGC 869

Qy         89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108

Db        870 CGTGGGCGCGTGCTGGTGCACTGCCAGGCGGGCATCTCGCGGTCGGCCACCATCTGCCTG 929

Qy        109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128

Db        930 GCCTACCTGATGATGAAGAAACGGGTGAGGCTGGAGGAGGCCTTCGAGTTCGTTAAGCAG 989

Qy        129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148

Db        990 CGCCGCAGCATCATCTCGCCCAACTTCAGCTTCATGGGGCAGCTGCTGCAGTTCGAGTCC 1049

Qy        149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168

Db       1050 CAGGTGCTGGCCACGTCCTGTGCTGCGGAGGCTGCTAGC---------- 1088

Qy        169 GluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrPro 188

Db       1089 ------CCCTCGGGACCCCTG----------GGGGAGCGGGGCAAGACCCCC 1124

Qy        189 LeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHis 208

Db       1125 GCCACCCCC----------ACCTCGCAGTTCGTCTTCAGCTTTCCGGTC--- 1163

Qy        209 ProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeu 228

Db       1164 TCCGTGGGCGTGCACTCGGCCCCCAGCAGCCTGCCCTACCTG------CACAGCCCCATC 1217

Qy        229 ValGlnAlaLeuSer 233

Db       1218 ACCACCTCTCCCAGC 1232

RESULT 14
US-09-702-705-801
; Sequence 801, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C14
;  CURRENT APPLICATION NUMBER: US/09/702,705
;  CURRENT FILING DATE:  2000-10-30
;  NUMBER OF SEQ ID NOS:  1833
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 801
;   LENGTH: 1619
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-702-705-801

Alignment Scores:
Pred. No.:              5.05e-19        Length:         1619
Score:                  287.00          Matches:        73
Percent Similarity:     55.02%          Conservative:   42
Best Local Similarity:  34.93%          Mismatches:     69
Query Match:            10.76%          Indels:         25
DB:                     4               Gaps:           6

US-09-964-277-21 (1-517) x US-09-702-705-801 (1-1619)

Qy         29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48

Db        365 AGAGACATGCTGGACGCCCTGGGCATCACGGCTCTGTTGAATGTCTCCTCGGACTGCCCA 424

Qy         49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68

Db        425 AAC---CACTTTGAAGGACACTATCAGTACAAGTGCATCCCAGTGGAAGATAACCACAAG 481

Qy         69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88

Db        482 GCCGACATCAGCTCCTGGTTCATGGAAGCCATAGAGTACATCGATGCCGTGAAGGACTGC 541

Qy         89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108

Db        542 CGTGGGCGCGTGCTGGTGCACTGCCAGGCGGGCATCTCGCGGTCGGCCACCATCTGCCTG 601

Qy        109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128

Db        602 GCCTACCTGATGATGAAGAAACGGGTGAGGCTGGAGGAGGCCTTCGAGTTCGTTAAGCAG 661

Qy        129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148

Db        662 CGCCGCAGCATTATCTCGCCCAACTTCAGCTTCATGGGGCAGCTGCTGCAGTTCGAGTCC 721

Qy        149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168

Db        722 CAGGTGCTGGCCACGTCCTGTGCTGCGGAGGCTGCTAGC---------- 760

Qy        169 GluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrPro 188

Db        761 ------CCCTCGGGACCCCTG----------CGGGAGCGGGGCAAGACCCCC 796

Qy        189 LeuSer-ProProCysAlaAspSerAlaThr------SerGluAlaAlaGlyGlnArgPr 206

Db        797 GCCACCCCCACCTCGCAGTTCGTCTTCAGCTTTCCGGTCTCCGTGGGCGTGCACTCGGCC 856

Qy        206 oValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSe 226

Db        857 C------CCAGCAGCCTGCCCTACCTGCACAGCCCCATCACCACCTCTC---------- 899

Qy        226 rProLeuValGlnAlaLeuSerGly 234

Db        900 -CCAGCTGTTAGAGCCGCCCTGGGG 923

RESULT 15
US-09-736-457-801
; Sequence 801, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Wang, Aijun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C15
;  CURRENT APPLICATION NUMBER: US/09/736,457
;  CURRENT FILING DATE:  2000-12-13
;  NUMBER OF SEQ ID NOS:  1864
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 801
;   LENGTH: 1619
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-736-457-801

Alignment Scores:
Pred. No.:              5.05e-19        Length:         1619
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Score:	287.00	Matches:	73
Percent Similarity:	55.02%	Conservative:	42
Best Local Similarity:	34.93%	Mismatches:	69
Query Match:	10.76%	Indels:	25
DB:	4	Gaps:	6

US-09-964-277-21 (1-517) x US-09-736-457-801 (1-1619)

```
Qy         29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
              ::::::::::::         ||||||      :::||||||   |||:::   ||||||
Db        365 AGAGACATGCTGGACGCCCTGGGCATCACGGCTCTGTTGAATGTCTCCTCGGACTGCCCA 424

Qy         49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
                    |||                  :::      :::||||||   |||:::
Db        425 AAC---CACTTTGAAGGACACTATCAGTACAAGTGCATCCCAGTGGAAGATAACCACAAG 481

Qy         69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
                  |||       |||       :::::::::::::::|||:::       |||
Db        482 GCCGACATCAGCTCCTGGTTCATGGAAGCCATAGAGTACATCGATGCCGTGAAGGACTGC 541

Qy         89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
                 |||   ||||||||||||||   |||||||||||||||||||||||||   :::
Db        542 CGTGGGCGCGTGCTGGTGCACTGCCAGGCGGGCATCTCGCGGTCGGCCACCATCTGCCTG 601

Qy        109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128
              ||||||:::|||   :::      :::   |||:::||||||:::   |||||||||:::
Db        602 GCCTACCTGATGATGAAGAAACGGGTGAGGCTGGAGGAGGCCTTCGAGTTCGTTAAGCAG 661

Qy        129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
              :::|||      ||||||||||||||:::|||:::||||||||||||   :::|||
Db        662 CGCCGCAGCATTATCTCGCCCAACTTCAGCTTCATGGGGCAGCTGCTGCAGTTCGAGTCC 721

Qy        149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168
              ::::::          :::   |||:::        |||
Db        722 CAGGTGCTGGCCACGTCCTGTGCTGCGGAGGCTGCTAGC---------------------- 760

Qy        169 GluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrPro 188
                   |||:::   |||:::                     ::::::   :::||||||
Db        761 ------CCCTCGGGACCCCTG-----------------CGGGAGCGGGGCAAGACCCCC 796

Qy        189 LeuSer-ProProCysAlaAspSerAlaThr------SerGluAlaAlaGlyGlnArgPr 206
                 ::: ||||||   :::   |||:::         |||      |||      |||||
Db        797 GCCACCCCCACCTCGCAGTTCGTCTTCAGCTTTCCGGTCTCCGTGGGCGTGCACTCGGCC 856

Qy        206 oValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSe 226
              |      ||||||:::   |||:::      :::      |||   |||
Db        857 C------CCAGCAGCCTGCCCTACCTGCACAGCCCCATCACCACCTCTC---------- 899

Qy        226 rProLeuValGlnAlaLeuSerGly 234
               |||   |||:::|||      |||
Db        900 -CCAGCTGTTAGAGCCGCCCTGGGG 923
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Search completed: September 1, 2005, 11:43:04
Job time : 396 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 31, 2005, 11:02:23 ; Search time 159 Seconds
(without alignments)
24.712 Million cell updates/sec

Title: US-09-964-277-16
Perfect score: 52
Sequence: 1 VHCLAGISRS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	52	100.0	10	9	US-09-964-277-16	Sequence 16, Appl
2	52	100.0	23	18	US-10-029-345A-103	Sequence 103, App
3	52	100.0	23	18	US-10-029-345A-144	Sequence 144, App
4	52	100.0	41	9	US-09-964-277-13	Sequence 13, Appl
5	52	100.0	140	17	US-10-803-738-12	Sequence 12, Appl
6	52	100.0	140	18	US-10-029-345A-134	Sequence 134, App
7	52	100.0	141	17	US-10-803-738-7	Sequence 7, Appli
8	52	100.0	141	17	US-10-803-738-8	Sequence 8, Appli
9	52	100.0	155	9	US-09-964-277-6	Sequence 6, Appli
10	52	100.0	155	9	US-09-964-277-7	Sequence 7, Appli
11	52	100.0	155	9	US-09-955-732-6	Sequence 6, Appli
12	52	100.0	156	9	US-09-964-277-3	Sequence 3, Appli
13	52	100.0	156	9	US-09-964-277-4	Sequence 4, Appli
14	52	100.0	156	9	US-09-955-732-3	Sequence 3, Appli
15	52	100.0	156	9	US-09-955-732-4	Sequence 4, Appli
16	52	100.0	167	14	US-10-346-356-13	Sequence 13, Appl
17	52	100.0	168	9	US-09-775-925-24	Sequence 24, Appl
18	52	100.0	168	9	US-09-847-519A-9	Sequence 9, Appli
19	52	100.0	168	14	US-10-314-058-13	Sequence 13, Appl
20	52	100.0	168	14	US-10-405-808-15	Sequence 15, Appl
21	52	100.0	168	15	US-10-655-073-15	Sequence 15, Appl
22	52	100.0	168	17	US-10-962-126-24	Sequence 24, Appl
23	52	100.0	168	17	US-10-644-554-16	Sequence 16, Appl
24	52	100.0	168	18	US-10-658-661-12	Sequence 12, Appl
25	52	100.0	169	14	US-10-346-356-12	Sequence 12, Appl
26	52	100.0	169	14	US-10-346-356-15	Sequence 15, Appl
27	52	100.0	170	9	US-09-775-925-23	Sequence 23, Appl
28	52	100.0	170	9	US-09-775-925-26	Sequence 26, Appl
29	52	100.0	170	9	US-09-847-519A-8	Sequence 8, Appli
30	52	100.0	170	9	US-09-847-519A-11	Sequence 11, Appl
31	52	100.0	170	14	US-10-314-058-12	Sequence 12, Appl
32	52	100.0	170	14	US-10-314-058-14	Sequence 14, Appl
33	52	100.0	170	14	US-10-405-808-14	Sequence 14, Appl
34	52	100.0	170	14	US-10-405-808-16	Sequence 16, Appl
35	52	100.0	170	15	US-10-655-073-14	Sequence 14, Appl
36	52	100.0	170	15	US-10-655-073-16	Sequence 16, Appl
37	52	100.0	170	17	US-10-962-126-23	Sequence 23, Appl
38	52	100.0	170	17	US-10-962-126-26	Sequence 26, Appl
39	52	100.0	170	17	US-10-644-554-15	Sequence 15, Appl
40	52	100.0	170	17	US-10-644-554-17	Sequence 17, Appl
41	52	100.0	170	18	US-10-658-661-11	Sequence 11, Appl
42	52	100.0	170	18	US-10-658-661-13	Sequence 13, Appl
43	52	100.0	189	9	US-09-925-299-842	Sequence 842, App
44	52	100.0	189	10	US-09-925-299-842	Sequence 842, App
45	52	100.0	302	18	US-10-029-345A-191	Sequence 191, App
46	52	100.0	322	14	US-10-060-065-33	Sequence 33, Appl
47	52	100.0	322	14	US-10-059-585-54	Sequence 54, Appl
48	52	100.0	381	14	US-10-184-832-2	Sequence 2, Appli
49	52	100.0	381	18	US-10-029-345A-111	Sequence 111, App
50	52	100.0	419	16	US-10-472-380-2	Sequence 2, Appli
51	52	100.0	501	15	US-10-072-012-702	Sequence 702, App
52	52	100.0	517	9	US-09-964-277-21	Sequence 21, Appl
53	52	100.0	625	15	US-10-072-012-699	Sequence 699, App
54	52	100.0	625	18	US-10-029-345A-39	Sequence 39, Appl
55	52	100.0	625	18	US-10-029-345A-110	Sequence 110, App
56	52	100.0	662	15	US-10-072-012-258	Sequence 258, App
57	52	100.0	663	15	US-10-072-012-700	Sequence 700, App
58	52	100.0	663	18	US-10-029-345A-40	Sequence 40, Appl
59	52	100.0	664	18	US-10-029-345A-190	Sequence 190, App
60	52	100.0	665	9	US-09-816-494-2	Sequence 2, Appli
61	52	100.0	665	9	US-09-964-277-2	Sequence 2, Appli
62	52	100.0	665	15	US-10-094-749-2312	Sequence 2312, Ap
63	52	100.0	665	15	US-10-377-072-26	Sequence 26, Appl
64	52	100.0	665	15	US-10-072-012-680	Sequence 680, App
65	52	100.0	665	15	US-10-072-012-681	Sequence 681, App
66	52	100.0	665	15	US-10-168-506-14	Sequence 14, Appl
67	52	100.0	665	15	US-10-343-357-7	Sequence 7, Appli
68	52	100.0	665	15	US-10-257-026-2	Sequence 2, Appli
69	52	100.0	665	16	US-10-648-593-240	Sequence 240, App
70	52	100.0	665	16	US-10-648-593-247	Sequence 247, App
71	52	100.0	665	16	US-10-377-072-26	Sequence 26, Appl
72	52	100.0	665	16	US-10-370-715B-262	Sequence 262, App
73	52	100.0	665	17	US-10-838-181-14	Sequence 14, Appl
74	52	100.0	665	18	US-10-029-345A-42	Sequence 42, Appl
75	52	100.0	665	18	US-10-029-345A-109	Sequence 109, App
76	52	100.0	665	18	US-10-029-345A-148	Sequence 148, App
77	52	100.0	672	15	US-10-296-115-1259	Sequence 1259, Ap
78	52	100.0	680	15	US-10-072-012-256	Sequence 256, App
79	52	100.0	690	15	US-10-072-012-679	Sequence 679, App
80	52	100.0	690	15	US-10-072-012-703	Sequence 703, App
81	52	100.0	690	15	US-10-425-114-54204	Sequence 54204, A
82	51	98.1	10	18	US-10-658-661-3	Sequence 3, Appli
83	51	98.1	92	16	US-10-425-115-335209	Sequence 335209,
84	51	98.1	138	17	US-10-803-738-5	Sequence 5, Appli

85	51	98.1	140	18	US-10-029-345A-135	Sequence 135, App
86	51	98.1	141	17	US-10-803-738-9	Sequence 9, Appli
87	51	98.1	145	18	US-10-658-661-19	Sequence 19, Appl
88	51	98.1	156	9	US-09-964-277-5	Sequence 5, Appli
89	51	98.1	156	9	US-09-955-732-5	Sequence 5, Appli
90	51	98.1	157	9	US-09-775-925-25	Sequence 25, Appl
91	51	98.1	157	9	US-09-847-519A-10	Sequence 10, Appl
92	51	98.1	157	17	US-10-962-126-25	Sequence 25, Appl
93	51	98.1	162	15	US-10-104-047-3471	Sequence 3471, Ap
94	51	98.1	179	15	US-10-296-115-1179	Sequence 1179, Ap
95	51	98.1	184	14	US-10-151-320-15	Sequence 15, Appl
96	51	98.1	184	14	US-10-287-806-2	Sequence 2, Appli
97	51	98.1	184	15	US-10-264-237-2811	Sequence 2811, Ap
98	51	98.1	184	15	US-10-072-012-428	Sequence 428, App
99	51	98.1	184	15	US-10-072-012-429	Sequence 429, App
100	51	98.1	184	15	US-10-072-012-430	Sequence 430, App

ALIGNMENTS

RESULT 1
US-09-964-277-16
; Sequence 16, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-16

Query Match 100.0%; Score 52; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
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Db 1 VHCLAGISRS 10

RESULT 2
US-10-029-345A-103
; Sequence 103, Application US/10029345A
; Publication No. US20050130286A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
; FILE REFERENCE: D0072.NP
; CURRENT APPLICATION NUMBER: US/10/029,345A
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/256,868
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/280,186
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/287,735
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 60/295,848
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/300,465
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103
; LENGTH: 23
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-029-345A-103

Query Match 100.0%; Score 52; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
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Db 6 VHCLAGISRS 15

RESULT 3
US-10-029-345A-144
; Sequence 144, Application US/10029345A
; Publication No. US20050130286A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
; FILE REFERENCE: D0072.NP
; CURRENT APPLICATION NUMBER: US/10/029,345A
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/256,868
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/280,186
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/287,735
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 60/295,848
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/300,465
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 144
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-345A-144

Query Match 100.0%; Score 52; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
||||||||||
Db 6 VHCLAGISRS 15

RESULT 4
US-09-964-277-13
; Sequence 13, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-13

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Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VHCLAGISRS 10
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Db         11 VHCLAGISRS 20


RESULT 5
US-10-803-738-12
; Sequence 12, Application US/10803738
; Publication No. US20050014222A1
; GENERAL INFORMATION:
;  APPLICANT: Belmont, John
;  APPLICANT:  Fletcher, Frederick
;  APPLICANT:  Chen, Alice
;  APPLICANT:  Jurecic, Roland
;  APPLICANT:  Colicos, Suzanne
;  APPLICANT:  Tan, Tse-Hua
;  APPLICANT:  Zhou, Guisheng
;  TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways
;  FILE REFERENCE: 99-383-B
;  CURRENT APPLICATION NUMBER: US/10/803,738
;  CURRENT FILING DATE:  2004-03-18
;  PRIOR APPLICATION NUMBER: US/09/665,819A
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US 60/155,068
;  PRIOR FILING DATE: 1999-09-21
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 140
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: MH3/6
US-10-803-738-12

  Query Match           100.0%;  Score 52;  DB 17;  Length 140;
  Best Local Similarity  100.0%;  Pred. No. 0.098;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         84 VHCLAGISRS 93


RESULT 6
US-10-029-345A-134
; Sequence 134, Application US/10029345A
; Publication No. US20050130286A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
;  FILE REFERENCE: D0072.NP
;  CURRENT APPLICATION NUMBER: US/10/029,345A
;  CURRENT FILING DATE:  2001-12-20
;  PRIOR APPLICATION NUMBER: US 60/256,868
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: US 60/280,186
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/287,735
;  PRIOR FILING DATE: 2001-05-01
;  PRIOR APPLICATION NUMBER: US 60/295,848
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/300,465
;  PRIOR FILING DATE: 2001-06-25
;  NUMBER OF SEQ ID NOS: 208
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 134
;   LENGTH: 140
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-029-345A-134

  Query Match           100.0%;  Score 52;  DB 18;  Length 140;
  Best Local Similarity  100.0%;  Pred. No. 0.098;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         85 VHCLAGISRS 94


RESULT 7
US-10-803-738-7
; Sequence 7, Application US/10803738
; Publication No. US20050014222A1
; GENERAL INFORMATION:
;  APPLICANT: Belmont, John
;  APPLICANT:  Fletcher, Frederick
;  APPLICANT:  Chen, Alice
;  APPLICANT:  Jurecic, Roland
;  APPLICANT:  Colicos, Suzanne
;  APPLICANT:  Tan, Tse-Hua
;  APPLICANT:  Zhou, Guisheng
;  TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways
;  FILE REFERENCE: 99-383-B
;  CURRENT APPLICATION NUMBER: US/10/803,738
;  CURRENT FILING DATE:  2004-03-18
;  PRIOR APPLICATION NUMBER: US/09/665,819A
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US 60/155,068
;  PRIOR FILING DATE: 1999-09-21
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 141
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: rMKP-3
US-10-803-738-7

  Query Match           100.0%;  Score 52;  DB 17;  Length 141;
  Best Local Similarity  100.0%;  Pred. No. 0.098;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
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Db         85 VHCLAGISRS 94


RESULT 8
US-10-803-738-8
; Sequence 8, Application US/10803738
; Publication No. US20050014222A1
; GENERAL INFORMATION:
;  APPLICANT: Belmont, John
;  APPLICANT:  Fletcher, Frederick
;  APPLICANT:  Chen, Alice
;  APPLICANT:  Jurecic, Roland
;  APPLICANT:  Colicos, Suzanne
;  APPLICANT:  Tan, Tse-Hua
;  APPLICANT:  Zhou, Guisheng
;  TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways
;  FILE REFERENCE: 99-383-B
;  CURRENT APPLICATION NUMBER: US/10/803,738
;  CURRENT FILING DATE:  2004-03-18
;  PRIOR APPLICATION NUMBER: US/09/665,819A
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US 60/155,068
;  PRIOR FILING DATE: 1999-09-21
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 141
;   TYPE: PRT
;   ORGANISM: Artificial
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: rMKP-X
US-10-803-738-8

  Query Match             100.0%;  Score 52;  DB 17;  Length 141;
  Best Local Similarity   100.0%;  Pred. No. 0.098;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         85 VHCLAGISRS 94


RESULT 9
US-09-964-277-6
; Sequence 6, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.434
;  CURRENT APPLICATION NUMBER: US/09/964,277
;  CURRENT FILING DATE:  2001-09-25
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 155
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-964-277-6

  Query Match             100.0%;  Score 52;  DB 9;  Length 155;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         96 VHCLAGISRS 105


RESULT 10
US-09-964-277-7
; Sequence 7, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.434
;  CURRENT APPLICATION NUMBER: US/09/964,277
;  CURRENT FILING DATE:  2001-09-25
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 155
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-964-277-7

  Query Match             100.0%;  Score 52;  DB 9;  Length 155;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         96 VHCLAGISRS 105


RESULT 11
US-09-955-732-6
; Sequence 6, Application US/09955732
; Publication No. US20020182203A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.433
;  CURRENT APPLICATION NUMBER: US/09/955,732
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 155
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-955-732-6

  Query Match             100.0%;  Score 52;  DB 9;  Length 155;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         96 VHCLAGISRS 105


RESULT 12
US-09-964-277-3
; Sequence 3, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.434
;  CURRENT APPLICATION NUMBER: US/09/964,277
;  CURRENT FILING DATE:  2001-09-25
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 156
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-964-277-3

  Query Match             100.0%;  Score 52;  DB 9;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         97 VHCLAGISRS 106


RESULT 13
US-09-964-277-4
; Sequence 4, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.434
;  CURRENT APPLICATION NUMBER: US/09/964,277
;  CURRENT FILING DATE:  2001-09-25
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 156
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-964-277-4

  Query Match             100.0%;  Score 52;  DB 9;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
```

```
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         97 VHCLAGISRS 106


RESULT 14
US-09-955-732-3
; Sequence 3, Application US/09955732
; Publication No. US20020182203A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.433
;  CURRENT APPLICATION NUMBER: US/09/955,732
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 156
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-955-732-3

  Query Match           100.0%;  Score 52;  DB 9;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         97 VHCLAGISRS 106


RESULT 15
US-09-955-732-4
; Sequence 4, Application US/09955732
; Publication No. US20020182203A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.433
;  CURRENT APPLICATION NUMBER: US/09/955,732
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 156
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-955-732-4

  Query Match           100.0%;  Score 52;  DB 9;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         97 VHCLAGISRS 106


RESULT 16
US-10-346-356-13
; Sequence 13, Application US/10346356
; Publication No. US20030138931A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.416C1
;  CURRENT APPLICATION NUMBER: US/10/346,356
;  CURRENT FILING DATE:  2003-01-15
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 167
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-346-356-13

  Query Match           100.0%;  Score 52;  DB 14;  Length 167;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        108 VHCLAGISRS 117


RESULT 17
US-09-775-925-24
; Sequence 24, Application US/09775925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-12 AND DSP-13 DUAL-SPECIFICITY
;  TITLE OF INVENTION:  PHOSPHATASES
;  FILE REFERENCE:  200125.420
;  CURRENT APPLICATION NUMBER: US/09/775,925
;  CURRENT FILING DATE:  2001-02-01
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-775-925-24

  Query Match           100.0%;  Score 52;  DB 9;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        108 VHCLAGISRS 117


RESULT 18
US-09-847-519A-9
; Sequence 9, Application US/09847519A
; Patent No. US20020102693A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.422
;  CURRENT APPLICATION NUMBER: US/09/847,519A
;  CURRENT FILING DATE:  2001-05-01
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-847-519A-9

  Query Match           100.0%;  Score 52;  DB 9;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        108 VHCLAGISRS 117
```

```
RESULT 19
US-10-314-058-13
; Sequence 13, Application US/10314058
; Publication No. US20030119045A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.415C1
;  CURRENT APPLICATION NUMBER: US/10/314,058
;  CURRENT FILING DATE:  2002-12-05
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-314-058-13

  Query Match             100.0%;  Score 52;  DB 14;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        108 VHCLAGISRS 117


RESULT 20
US-10-405-808-15
; Sequence 15, Application US/10405808
; Publication No. US20030175829A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-4 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.410C1
;  CURRENT APPLICATION NUMBER: US/10/405,808
;  CURRENT FILING DATE:  2003-04-01
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-405-808-15

  Query Match             100.0%;  Score 52;  DB 14;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        108 VHCLAGISRS 117


RESULT 21
US-10-655-073-15
; Sequence 15, Application US/10655073
; Publication No. US20040043411A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.418C1
;  CURRENT APPLICATION NUMBER: US/10/655,073
;  CURRENT FILING DATE:  2003-09-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-655-073-15

  Query Match             100.0%;  Score 52;  DB 15;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        108 VHCLAGISRS 117


RESULT 22
US-10-962-126-24
; Sequence 24, Application US/10962126
; Publication No. US20050058650A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
;  TITLE OF INVENTION:  PHOSPHATASES
;  FILE REFERENCE: 200125.420C1
;  CURRENT APPLICATION NUMBER: US/10/962,126
;  CURRENT FILING DATE:  2004-10-08
;  PRIOR APPLICATION NUMBER: US 09/775,925
;  PRIOR FILING DATE: 2001-02-01
;  PRIOR APPLICATION NUMBER: US 60/179,886
;  PRIOR FILING DATE: 2000-02-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-962-126-24

  Query Match             100.0%;  Score 52;  DB 17;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        108 VHCLAGISRS 117


RESULT 23
US-10-644-554-16
; Sequence 16, Application US/10644554
; Publication No. US20050075489A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.413C1
;  CURRENT APPLICATION NUMBER: US/10/644,554
;  CURRENT FILING DATE:  2003-08-19
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-644-554-16

  Query Match             100.0%;  Score 52;  DB 17;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        108 VHCLAGISRS 117
```

```
RESULT 24
US-10-658-661-12
; Sequence 12, Application US/10658661
; Publication No. US20050176124A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-3 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.408C2
;  CURRENT APPLICATION NUMBER: US/10/658,661
;  CURRENT FILING DATE:  2003-09-08
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-658-661-12

  Query Match             100.0%;  Score 52;  DB 18;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        108 VHCLAGISRS 117


RESULT 25
US-10-346-356-12
; Sequence 12, Application US/10346356
; Publication No. US20030138931A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.416C1
;  CURRENT APPLICATION NUMBER: US/10/346,356
;  CURRENT FILING DATE:  2003-01-15
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-346-356-12

  Query Match             100.0%;  Score 52;  DB 14;  Length 169;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 26
US-10-346-356-15
; Sequence 15, Application US/10346356
; Publication No. US20030138931A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.416C1
;  CURRENT APPLICATION NUMBER: US/10/346,356
;  CURRENT FILING DATE:  2003-01-15
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-346-356-15

  Query Match             100.0%;  Score 52;  DB 14;  Length 169;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 27
US-09-775-925-23
; Sequence 23, Application US/09775925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-12 AND DSP-13 DUAL-SPECIFICITY
;  TITLE OF INVENTION:  PHOSPHATASES
;  FILE REFERENCE:  200125.420
;  CURRENT APPLICATION NUMBER: US/09/775,925
;  CURRENT FILING DATE:  2001-02-01
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-775-925-23

  Query Match             100.0%;  Score 52;  DB 9;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 28
US-09-775-925-26
; Sequence 26, Application US/09775925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
;  APPLICANT:  Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION:  DSP-12 AND DSP-13 DUAL-SPECIFICITY
;  TITLE OF INVENTION:  PHOSPHATASES
;  FILE REFERENCE:  200125.420
;  CURRENT APPLICATION NUMBER: US/09/775,925
;  CURRENT FILING DATE:  2001-02-01
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-775-925-26

  Query Match             100.0%;  Score 52;  DB 9;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 29
US-09-847-519A-8
; Sequence 8, Application US/09847519A
```

; Patent No. US20020102693A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.422
; CURRENT APPLICATION NUMBER: US/09/847,519A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-519A-8

Query Match 100.0%; Score 52; DB 9; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
||||||||||
Db 110 VHCLAGISRS 119

RESULT 30
US-09-847-519A-11
; Sequence 11, Application US/09847519A
; Patent No. US20020102693A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.422
; CURRENT APPLICATION NUMBER: US/09/847,519A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-519A-11

Query Match 100.0%; Score 52; DB 9; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
||||||||||
Db 110 VHCLAGISRS 119

RESULT 31
US-10-314-058-12
; Sequence 12, Application US/10314058
; Publication No. US20030119045A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415C1
; CURRENT APPLICATION NUMBER: US/10/314,058
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-058-12

Query Match 100.0%; Score 52; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
||||||||||
Db 110 VHCLAGISRS 119

RESULT 32
US-10-314-058-14
; Sequence 14, Application US/10314058
; Publication No. US20030119045A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415C1
; CURRENT APPLICATION NUMBER: US/10/314,058
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-058-14

Query Match 100.0%; Score 52; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
||||||||||
Db 110 VHCLAGISRS 119

RESULT 33
US-10-405-808-14
; Sequence 14, Application US/10405808
; Publication No. US20030175829A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-4 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.410C1
; CURRENT APPLICATION NUMBER: US/10/405,808
; CURRENT FILING DATE: 2003-04-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-405-808-14

Query Match 100.0%; Score 52; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
||||||||||
Db 110 VHCLAGISRS 119

RESULT 34
US-10-405-808-16
; Sequence 16, Application US/10405808
; Publication No. US20030175829A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-4 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.410C1

```
;  CURRENT APPLICATION NUMBER: US/10/405,808
;  CURRENT FILING DATE:  2003-04-01
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-405-808-16

  Query Match             100.0%;  Score 52;  DB 14;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 35
US-10-655-073-14
; Sequence 14, Application US/10655073
; Publication No. US20040043411A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.418C1
;  CURRENT APPLICATION NUMBER: US/10/655,073
;  CURRENT FILING DATE:  2003-09-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-655-073-14

  Query Match             100.0%;  Score 52;  DB 15;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 36
US-10-655-073-16
; Sequence 16, Application US/10655073
; Publication No. US20040043411A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.418C1
;  CURRENT APPLICATION NUMBER: US/10/655,073
;  CURRENT FILING DATE:  2003-09-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-655-073-16

  Query Match             100.0%;  Score 52;  DB 15;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 37
US-10-962-126-23
; Sequence 23, Application US/10962126
; Publication No. US20050058650A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
;  TITLE OF INVENTION:  PHOSPHATASES
;  FILE REFERENCE: 200125.420C1
;  CURRENT APPLICATION NUMBER: US/10/962,126
;  CURRENT FILING DATE:  2004-10-08
;  PRIOR APPLICATION NUMBER: US 09/775,925
;  PRIOR FILING DATE: 2001-02-01
;  PRIOR APPLICATION NUMBER: US 60/179,886
;  PRIOR FILING DATE: 2000-02-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-962-126-23

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
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Db        110 VHCLAGISRS 119


RESULT 38
US-10-962-126-26
; Sequence 26, Application US/10962126
; Publication No. US20050058650A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
;  TITLE OF INVENTION:  PHOSPHATASES
;  FILE REFERENCE: 200125.420C1
;  CURRENT APPLICATION NUMBER: US/10/962,126
;  CURRENT FILING DATE:  2004-10-08
;  PRIOR APPLICATION NUMBER: US 09/775,925
;  PRIOR FILING DATE: 2001-02-01
;  PRIOR APPLICATION NUMBER: US 60/179,886
;  PRIOR FILING DATE: 2000-02-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-962-126-26

  Query Match             100.0%;  Score 52;  DB 17;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 39
US-10-644-554-15
; Sequence 15, Application US/10644554
; Publication No. US20050075489A1
; GENERAL INFORMATION:
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;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.413C1
;  CURRENT APPLICATION NUMBER: US/10/644,554
;  CURRENT FILING DATE:  2003-08-19
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-644-554-15

  Query Match             100.0%;  Score 52;  DB 17;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 40
US-10-644-554-17
; Sequence 17, Application US/10644554
; Publication No. US20050075489A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.413C1
;  CURRENT APPLICATION NUMBER: US/10/644,554
;  CURRENT FILING DATE:  2003-08-19
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-644-554-17

  Query Match             100.0%;  Score 52;  DB 17;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 41
US-10-658-661-11
; Sequence 11, Application US/10658661
; Publication No. US20050176124A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-3 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.408C2
;  CURRENT APPLICATION NUMBER: US/10/658,661
;  CURRENT FILING DATE:  2003-09-08
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-658-661-11

  Query Match             100.0%;  Score 52;  DB 18;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 42
US-10-658-661-13
; Sequence 13, Application US/10658661
; Publication No. US20050176124A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-3 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.408C2
;  CURRENT APPLICATION NUMBER: US/10/658,661
;  CURRENT FILING DATE:  2003-09-08
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-658-661-13

  Query Match             100.0%;  Score 52;  DB 18;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db        110 VHCLAGISRS 119


RESULT 43
US-09-925-299-842
; Sequence 842, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA102
;  CURRENT APPLICATION NUMBER: US/09/925,299
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05883
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 842
;   LENGTH: 189
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-299-842

  Query Match             100.0%;  Score 52;  DB 9;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
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Db         99 VHCLAGISRS 108


RESULT 44
US-09-925-299-842
; Sequence 842, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA102
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;  CURRENT APPLICATION NUMBER: US/09/925,299
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05883
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 842
;   LENGTH: 189
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-299-842

  Query Match             100.0%;  Score 52;  DB 10;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
              ||||||||||
Db         99 VHCLAGISRS 108


RESULT 45
US-10-029-345A-191
; Sequence 191, Application US/10029345A
; Publication No. US20050130286A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
;  FILE REFERENCE: D0072.NP
;  CURRENT APPLICATION NUMBER: US/10/029,345A
;  CURRENT FILING DATE:  2001-12-20
;  PRIOR APPLICATION NUMBER: US 60/256,868
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: US 60/280,186
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/287,735
;  PRIOR FILING DATE: 2001-05-01
;  PRIOR APPLICATION NUMBER: US 60/295,848
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/300,465
;  PRIOR FILING DATE: 2001-06-25
;  NUMBER OF SEQ ID NOS: 208
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 191
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-029-345A-191

  Query Match             100.0%;  Score 52;  DB 18;  Length 302;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VHCLAGISRS 10
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Db        242 VHCLAGISRS 251


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Perfect score: 3332
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3332	100.0	3332	9	US-09-964-277-20	Sequence 20, Appl
2	3158	94.8	3496	9	US-09-964-277-1	Sequence 1, Appli
3	3145	94.4	3625	18	US-10-425-114-26234	Sequence 26234, A
4	3133.4	94.0	3521	20	US-10-370-715B-261	Sequence 261, App
5	3118.8	93.6	3766	18	US-10-343-357-17	Sequence 17, Appl
6	3106.2	93.2	5450	22	US-10-029-345A-108	Sequence 108, App
7	3106.2	93.2	5450	22	US-10-029-345A-147	Sequence 147, App
8	2950	88.5	3544	9	US-09-816-494-1	Sequence 1, Appli
9	2950	88.5	3544	17	US-10-377-072-25	Sequence 25, Appl
10	2950	88.5	3544	19	US-10-377-072-25	Sequence 25, Appl
11	2950	88.5	5145	20	US-10-357-930-20824	Sequence 20824, A
12	2950	88.5	5145	20	US-10-357-930-20969	Sequence 20969, A
13	2950	88.5	5145	20	US-10-357-930-21071	Sequence 21071, A
14	2950	88.5	5145	20	US-10-357-930-21083	Sequence 21083, A
15	2950	88.5	5145	20	US-10-357-930-21303	Sequence 21303, A
16	2950	88.5	5145	20	US-10-357-930-21307	Sequence 21307, A
17	2950	88.5	5145	20	US-10-357-930-22820	Sequence 22820, A
18	2950	88.5	5145	20	US-10-357-930-26669	Sequence 26669, A
19	2950	88.5	5145	20	US-10-357-930-26815	Sequence 26815, A
20	2950	88.5	5145	20	US-10-357-930-26912	Sequence 26912, A
21	2950	88.5	5145	20	US-10-357-930-26923	Sequence 26923, A
22	2950	88.5	5145	20	US-10-357-930-27145	Sequence 27145, A
23	2950	88.5	5145	20	US-10-357-930-27149	Sequence 27149, A
24	2950	88.5	5145	20	US-10-357-930-28675	Sequence 28675, A
25	2924.6	87.8	5111	22	US-10-029-345A-41	Sequence 41, Appl
26	2766.4	83.0	4790	19	US-10-648-593-115	Sequence 115, App
27	2710	81.3	3059	18	US-10-257-026-1	Sequence 1, Appli
28	2602.8	78.1	2966	18	US-10-296-115-520	Sequence 520, App
29	2390.8	71.8	2732	18	US-10-168-506-2	Sequence 2, Appli
30	2390.8	71.8	2732	21	US-10-838-181-2	Sequence 2, Appli
31	1795.4	53.9	1916	17	US-10-108-260A-2429	Sequence 2429, Ap
32	1762.4	52.9	2102	17	US-10-094-749-673	Sequence 673, App
33	1742	52.3	2200	18	US-10-072-012-255	Sequence 255, App
34	1712.4	51.4	2071	18	US-10-072-012-257	Sequence 257, App
35	1660	49.8	1998	9	US-09-816-494-3	Sequence 3, Appli
36	1660	49.8	1998	17	US-10-377-072-27	Sequence 27, Appl
37	1660	49.8	1998	19	US-10-377-072-27	Sequence 27, Appl
38	1638.2	49.2	2756	22	US-10-029-345A-113	Sequence 113, App
39	886.8	26.6	2558	17	US-10-104-047-1750	Sequence 1750, Ap
40	595	17.9	787	17	US-10-220-891-85	Sequence 85, Appl
41	537.4	16.1	877	9	US-09-764-853-158	Sequence 158, App
c 42	417.2	12.5	425	20	US-10-357-930-10717	Sequence 10717, A
c 43	415.2	12.5	467	20	US-10-357-930-31909	Sequence 31909, A
c 44	415.2	12.5	467	20	US-10-357-930-40868	Sequence 40868, A
c 45	415.2	12.5	467	20	US-10-357-930-41017	Sequence 41017, A

ALIGNMENTS

RESULT 1
US-09-964-277-20
; Sequence 20, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 3332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-20

Query Match 100.0%; Score 3332; DB 9; Length 3332;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGAGAAGGAGAAGATAATATACTGAAAAGAAGAGGAGGAGGAGAGCGACGGGACGGGAC 60
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Db 1 GAGAGAAGGAGAAGATAATATACTGAAAAGAAGAGGAGGAGGAGAGCGACGGGACGGGAC 60

Qy 61 GCGAGCGGGAGCGCAGCCGCCCTCTCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGC 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GCGAGCGGGAGCGCAGCCGCCCTCTCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGC 120

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Qy      121 GAGGGGGGCCCGAGGGGAGACGCCGTGACAACTTTCGTTTCCCTCTGAGGGAATTGGGAG 180
Db      121 GAGGGGGGCCCGAGGGGAGACGCCGTGACAACTTTCGTTTCCCTCTGAGGGAATTGGGAG 180

Qy      181 GTCGGCGGCCCCAAAAGCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGT 240
Db      181 GTCGGCGGCCCCAAAAGCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGT 240

Qy      241 AAAGAATGATGTAATGCGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCC 300
Db      241 AAAGAATGATGTAATGCGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCC 300

Qy      301 AGTCATCTCTTTATGAATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGA 360
Db      301 AGTCATCTCTTTATGAATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGA 360

Qy      361 GCACATCAACGGGAAAGAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTT 420
Db      361 GCACATCAACGGGAAAGAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTT 420

Qy      421 TAACTCTCCTTTTGCCAGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGT 480
Db      421 TAACTCTCCTTTTGCCAGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGT 480

Qy      481 GGCTGAGCCTTTGAGCACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGG 540
Db      481 GGCTGAGCCTTTGAGCACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGG 540

Qy      541 AAAAGAGGACTTATTGTTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAG 600
Db      541 AAAAGAGGACTTATTGTTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAG 600

Qy      601 AGGTTGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCA 660
Db      601 AGGTTGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCA 660

Qy      661 TTTGTGGAATACAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTT 720
Db      661 TTTGTGGAATACAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTT 720

Qy      721 ATGAAGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCG 780
Db      721 ATGAAGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCG 780

Qy      781 AAACATAAGGTTGACATTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAA 840
Db      781 AAACATAAGGTTGACATTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAA 840

Qy      841 GATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAG 900
Db      841 GATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAG 900

Qy      901 AGCTTCAACTCTGTTCACCTGCTTGCAGGAGCTGATGCAGCAGAATGGGATTGGTTATGT 960
Db      901 AGCTTCAACTCTGTTCACCTGCTTGCAGGAGCTGATGCAGCAGAATGGGATTGGTTATGT 960

Qy      961 GTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCG 1020
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Qy     1021 TGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGA 1080
Db     1021 TGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGA 1080

Qy     1081 TTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGAT 1140
Db     1081 TTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGAT 1140

Qy     1141 CTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGA 1200
Db     1141 CTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGA 1200

Qy     1201 TGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCT 1260
Db     1201 TGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCT 1260

Qy     1261 GGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAA 1320
Db     1261 GGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAA 1320

Qy     1321 GAGCAAACTCAAGCTGCTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGA 1380
Db     1321 GAGCAAACTCAAGCTGCTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGA 1380

Qy     1381 GGGTGGACAGAAAAGCGAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGA 1440
Db     1381 GGGTGGACAGAAAAGCGAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGA 1440

Qy     1441 GGCAGCAGGACAAAGGCCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCC 1500
Db     1441 GGCAGCAGGACAAAGGCCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCC 1500

Qy     1501 GTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGA 1560
Db     1501 GTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGA 1560

Qy     1561 CAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTC 1620
Db     1561 CAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTC 1620

Qy     1621 ATATTCAGCCAGCATGGCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGA 1680
Db     1621 ATATTCAGCCAGCATGGCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGA 1680

Qy     1681 ATACTACAAACCTTCCACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGT 1740
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Qy     1741 TCAGGAACTATCGGAGCAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCC 1800
Db     1741 TCAGGAACTATCGGAGCAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCC 1800

Qy     1801 CAAGAAGCTGCAGACCGCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAG 1860
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Qy     1861 AACCAGCAGCAGTGGCACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAG 1920
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Qy     1921 CGTGGAGGACAATTACCACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCT 1980
Db     1921 CGTGGAGGACAATTACCACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCT 1980

Qy     1981 CACGAAGTCTGCTGGCCTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGAC 2040
Db     1981 CACGAAGTCTGCTGGCCTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGAC 2040

Qy     2041 CTCTACCCCTTCCCTGACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTC 2100
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Qy     2101 TGCCTCAGCCATCTACGGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCC 2160
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Db       2341 AGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCCTGAGAAGA 2400

Qy       2401 AAGACACTTGTGACTTCTATAGACAATTTTTTTTTCTTGTTCACAAAAAAATTCCCTGTA 2460
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Db       2401 AAGACACTTGTGACTTCTATAGACAATTTTTTTTTCTTGTTCACAAAAAAATTCCCTGTA 2460

Qy       2461 AATCTGAAATATATATATGTACATACATATATATTTTTGGAAAATGGAGCTATGGTGTAA 2520
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 AATCTGAAATATATATATGTACATACATATATATTTTTGGAAAATGGAGCTATGGTGTAA 2520

Qy       2521 AAGCAACAGGTGGATCAACCCAGTTGTTACTCTCTTAACATCTGCATTTGAGAGATCAGC 2580
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Qy       2581 TAATACTTCTCTCAACAAAAATGGAAGGGCAGATGCTAGAATCCCCCCTAGACGGAGGAA 2640
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Qy       2641 AACCATTTTATTCAGTGAATTACACATCCTCTTGTTCTTAAAAAAGCAAGTGTCTTTGGT 2700
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Db       2761 AGTCTTTGTCCGGACCCTTCCATAGTACACCTTAGCGCTGAGACTGAGCCAGCTTGGGGG 2820

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Db       2941 TGCTGGACGGACCATTAGGGGCCTTGCCAAGGTCTACCTTAGAGCAAACCCAGTACCTCA 3000

Qy       3001 GACAGGAAAGTCGGGGCTTTGACCACTACCATATCTGGTAGCCCATTTTCTAGGCATTGT 3060
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Db       3001 GACAGGAAAGTCGGGGCTTTGACCACTACCATATCTGGTAGCCCATTTTCTAGGCATTGT 3060

Qy       3061 GAATAGGTAGGTAGCTAGTCACACTTTTCAGACCAATTCAAACTGTCTATGCACAAAATT 3120
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Qy       3121 CCCGTGGGCCTAGATGGAGATAATTTTTTTTTCTTCTCAGCTTTATGAAGAGAAGGGAAA 3180
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RESULT 2

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US-09-964-277-1
; Sequence 1, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.434
;  CURRENT APPLICATION NUMBER: US/09/964,277
;  CURRENT FILING DATE:  2001-09-25
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3496
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-964-277-1

  Query Match            94.8%;  Score 3158;  DB 9;  Length 3496;
  Best Local Similarity  95.3%;  Pred. No. 0;
  Matches 3332;  Conservative    0;  Mismatches    0;  Indels  164;  Gaps    1;

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Qy        721 ATGAAGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCG 780
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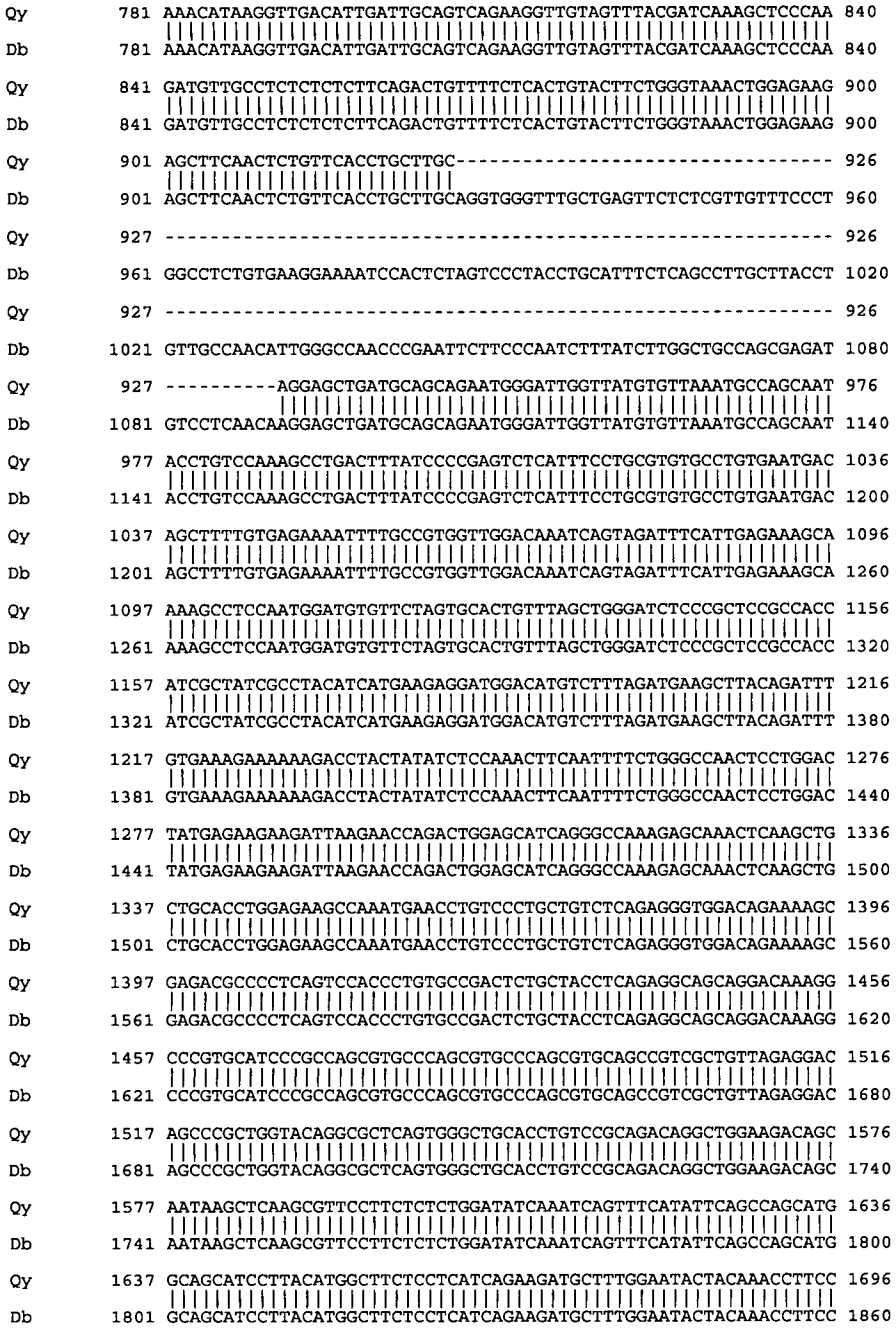
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Qy 901 AGCTTCAACTCTGTTCACCTGCTTGC---------- 926
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Qy 927 ---------- 926
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Db 1081 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 1140
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Qy 1577 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1636
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; Sequence 26234, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26234
;   LENGTH: 3625
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
US-10-425-114-26234

  Query Match             94.4%;  Score 3145;  DB 18;  Length 3625;
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  Matches 3330;  Conservative    0;  Mismatches    0;  Indels  165;  Gaps    2;

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Db         312 TCGGCGGCCCCAAAAGCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTA 371

Qy         242 AAGAATGATGTAATGCGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCA 301

Db         372 AAGAATGATGTAATGCGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCA 431

Qy         302 GTCATCTCTTTATGAATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAG 361

Db         432 GTCATCTCTTTATGAATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAG 491

Qy         362 CACATCAACGGGAAAGAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTT 421

Db         492 CACATCAACGGGAAAGAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTT 551

Qy         422 AACTCTCCTTTTGCCAGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGTG 481

Db         552 AACTCTCCTTTTGCCAGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGTG 611

Qy         482 GCTGAGCCTTTGAGCACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGA 541

Db         612 GCTGAGCCTTTGAGCACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGA 671

Qy         542 AAAGAGGACTTATTGTTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGA 601

Db         672 AAAGAGGACTTATTGTTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGA 731

Qy         602 GGTTGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCAT 661

Db         732 GGTTGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCAT 791

Qy         662 TTGTGGAATACAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTA 721

Db         792 TTGTGGAATACAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTA 851

Qy         722 TGAAGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGA 781

Db         852 TGAAGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGA 911

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Db         912 AACATAAGGTTGACATTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAG 971

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Db         972 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 1031

Qy         902 GCTTCAACTCTGTTCACCTGCTTGC---------------------------------- 926

Db        1032 GCTTCAACTCTGTTCACCTGCTTGCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTG 1091

Qy         927 ---------------------------------------------------------- 926

Db        1092 GCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTG 1151

Qy         927 ---------------------------------------------------------- 926

Db        1152 TTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATG 1211

Qy         927 ---------AGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATA 977

Db        1212 TCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATA 1271

Qy         978 CCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACA 1037
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Db      1272 CCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACA 1331
Qy      1038 GCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAA 1097
Db      1332 GCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAA 1391
Qy      1098 AAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCA 1157
Db      1392 AAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCA 1451
Qy      1158 TCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTG 1217
Db      1452 TCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTG 1511
Qy      1218 TGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACT 1277
Db      1512 TGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACT 1571
Qy      1278 ATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGC 1337
Db      1572 ATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGC 1631
Qy      1338 TGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCG 1397
Db      1632 TGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCG 1691
Qy      1398 AGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGC 1457
Db      1692 AGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGC 1751
Qy      1458 CCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACA 1517
Db      1752 CCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACA 1811
Qy      1518 GCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCA 1577
Db      1812 GCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCA 1871
Qy      1578 ATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATGG 1637
Db      1872 ATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATGG 1931
Qy      1638 CAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCA 1697
Db      1932 CAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCA 1991
Qy      1698 CTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGC 1757
Db      1992 CTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGC 2051
Qy      1758 AGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCG 1817
Db      2052 AGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCG 2111
Qy      1818 CCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCA 1877
Db      2112 CCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCA 2171
Qy      1878 CCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACC 1937
Db      2172 CCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACC 2231
Qy      1938 ACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCC 1997
Db      2232 ACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCC 2291
Qy      1998 TGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGA 2057
Db      2292 TGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGA 2351
Qy      2058 CCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACG 2117
Db      2352 CCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACG 2411
Qy      2118 GAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAG 2177
Db      2412 GAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAG 2471
Qy      2178 TCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGC 2237
Db      2472 TCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGC 2531
Qy      2238 ATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAG 2297
Db      2532 ATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAG 2591
Qy      2298 AGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTA 2357
Db      2592 AGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTA 2651
Qy      2358 GCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTC 2417
Db      2652 GCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTC 2711
Qy      2418 TATAGACAATTTTTTTTTTCTTGTTCACAAAAAAATTCCCTGTAAATCTGAAATATATATA 2477
Db      2712 TATAGACAATTTTTTTTTTCTTGTTCACAAAAAAATTCCCTGTAAATCTGAAATATATATA 2771
Qy      2478 TGTACATACATATATATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCA 2537
Db      2772 TGTACATACATATATATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCA 2831
Qy      2538 ACCCAGTTGTTACTCTCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACA 2597
Db      2832 ACCCAGTTGTTACTCTCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACA 2891
Qy      2598 AAAATGGAAGGGCAGATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTG 2657
Db      2892 AAAATGGAAGGGCAGATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTG 2951
Qy      2658 AATTACACATCCTCTTGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCC 2717
Db      2952 AATTACACATCCTCTTGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCC 3011
Qy      2718 CCTACCATTTTCCACGTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCC 2777
Db      3012 CCTACCATTTT-CACGTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCC 3070
Qy      2778 TTCCATAGTACACCTTAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCT 2837
Db      3071 TTCCATAGTACACCTTAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCT 3130
Qy      2838 GTTAGGGACAGAGCCTAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCAC 2897
Db      3131 GTTAGGGACAGAGCCTAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCAC 3190
Qy      2898 AAACCCACGCTCACCTGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCATTA 2957
Db      3191 AAACCCACGCTCACCTGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCATTA 3250
Qy      2958 GGGGCCTTGCCAAGGTCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGC 3017
Db      3251 GGGGCCTTGCCAAGGTCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGC 3310
Qy      3018 TTTGACCACTACCATATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTA 3077
Db      3311 TTTGACCACTACCATATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTA 3370
Qy      3078 GTCACACTTTTCAGACCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGG 3137
Db      3371 GTCACACTTTTCAGACCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGG 3430
Qy      3138 AGATAATTTTTTTTTCTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCT 3197
Db      3431 AGATAATTTTTTTTTCTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCT 3490
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Qy       3198 GAACCACCAGGAACCTGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCT 3257
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Db       3491 GAACCACCAGGAACCTGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCT 3550

Qy       3258 ACCTCCCTCTTTGTAAATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAA 3317
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Db       3551 ACCTCCCTCTTTGTAAATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAA 3610

Qy       3318 GATGAACTTGGTTTC 3332
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RESULT 4
US-10-370-715B-261
; Sequence 261, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
;    Patin Docket Preview
;  APPLICANT: BODARY,SARAH C.
;  APPLICANT:  CLARK,HILLARY
;  APPLICANT:  BRISDELL,HUNTE
;  APPLICANT:  JACKMAN,JANET
;  APPLICANT:  SCHOENFELD,JILL R.
;  APPLICANT:  WILLIAMS,P. MICKEY
;  APPLICANT:  WOOD,WILLIAM I.
;  APPLICANT:  WU,THOMAS D.
;  TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
;  TITLE OF INVENTION:  Related Diseases
;  FILE REFERENCE: P1948R1-US
;  CURRENT APPLICATION NUMBER: US/10/370,715B
;  CURRENT FILING DATE:  2003-02-21
;  NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 261
;   LENGTH: 3521
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-370-715B-261

  Query Match             94.0%;  Score 3133.4;  DB 20;  Length 3521;
  Best Local Similarity   95.2%;  Pred. No. 0;
  Matches 3330;  Conservative    0;  Mismatches    1;  Indels  166;  Gaps    3;

Qy          1 GAGAGAAGGAGAAGATAATATACTGAAAAGAAGAGGAGGAGGAGAGCGACGGGACGGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 GAGAGAAGGAGAAGATAATATACTGAAAAGAAGAGGAGGAGGAGAGCGACGGGACGGGAC 62

Qy         61 GCGAGCGGGAGCGCAGCCGCCCTCTCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GCGAGCGGGAGCGCAGCCGCCCTCTCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGC 122

Qy        121 GAGGGGGGCCCGAGGGGAGACGCCGTGACAACTTTCGTTTCCCTCTGAGGGAATTGGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GAGGGGGGCCCGAGGGGAGACGCCGTGACAACTTTCGTTTCCCTCTGAGGGAATTGGGAG 182

Qy        181 GTCGGCGGCCCCAAAAGCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTCGGCGGCCCCAAAAGCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGT 242

Qy        241 AAAGAATGATGTAATGCGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCC 300
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGAATGATGTAATGCACTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCC 302

Qy        301 AGTCATCTCTTTATGAATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 AGTCATCTCTTTATGAATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGA 362

Qy        361 GCACATCAACGGGAAAGAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCACATCAACGGGAAAGAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTT 422

Qy        421 TAACTCTCCTTTTGCCAGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 TAACTCTCCTTTTGCCAGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGT 482

Qy        481 GGCTGAGCCTTTGAGCACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 GGCTGAGCCTTTGAGCACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGG 542

Qy        541 AAAAGAGGACTTATTGTTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 AAAAGAGGACTTATTGTTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAG 602

Qy        601 AGGTTGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGGTTGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCA 662

Qy        661 TTTGTGGAATACAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 TTTGTGGAATACAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTT 722

Qy        721 ATGAAGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCG 780
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Db        723 ATGAAGCGAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCG 782

Qy        781 AAACATAAGGTTGACATTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAA 840
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Db        783 AAACATAAGGTTGACATTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAA 842

Qy        841 GATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAG 900
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Db        843 GATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAG 902

Qy        901 AGCTTCAACTCTGTTCACCTGCTTGC---------------------------------- 926
              ||||||||||||||||||||||||||
Db        903 AGCTTCAACTCTGTTCACCTGCTTGCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 962

Qy        927 ---------------------------------------------------------- 926

Db        963 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 1022

Qy        927 ---------------------------------------------------------- 926

Db       1023 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 1082

Qy        927 ----------AGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 976
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Db       1083 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 1142

Qy        977 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 1036
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 1202

Qy       1037 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 1096
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Qy       1097 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1156
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1263 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1322

Qy       1157 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1216
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1323 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1382

Qy       1217 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1276
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1383 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1442

Qy       1277 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1336
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1443 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1502

Qy       1337 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1396
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Db       1503 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1562

Qy       1397 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1456
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1563 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1622

Qy       1457 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1516
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1623 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1682

Qy       1517 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1576
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Db       1683 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1742

Qy       1577 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1636
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1637 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1696
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Qy       1757 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 1816
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Qy       1817 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 1876
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Db       1983 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 2042

Qy       1877 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 1936
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Qy       1937 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 1996
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Db       2103 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 2162

Qy       1997 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 2056
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Db       2163 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 2222

Qy       2057 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 2116
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2223 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 2282

Qy       2117 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 2176
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2283 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 2342

Qy       2177 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 2236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2343 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 2402

Qy       2237 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2296
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2403 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2462

Qy       2297 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2356
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Db       2463 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2522

Qy       2357 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTT 2416
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2523 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTT 2582

Qy       2417 CTATAGACAATTTTTTTTTCTTGTTCACAAAAAAATTCCCTGTAAATCTGAAATATATAT 2476
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2583 CTATAGACAATTTTTTTTTCTTGTTCACAAAAAAATTCCCTGTAAATCTGAAATATATAT 2642

Qy       2477 ATGTACATACATATATATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATC 2536
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2643 ATGTACATACATATATATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATC 2702

Qy       2537 AACCCAGTT-GTTACTCTCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAA 2595
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2703 AACCCAGTTGGTTACTCTCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAA 2762

Qy       2596 CAAAAATGGAAGGGCAGATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAG 2655
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2763 CAAAAATGGAAGGGCAGATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAG 2822

Qy       2656 TGAATTACACATCCTCTTGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAAT 2715
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2823 TGAATTACACATCCTCTTGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAAT 2882

Qy       2716 CCCCTACCATTTTCCACGTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGAC 2775
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Db       2883 CCCCTACCATTTT-CACGTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGAC 2941

Qy       2776 CCTTCCATAGTACACCTTAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACC 2835
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2942 CCTTCCATAGTACACCTTAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACC 3001

Qy       2836 CTGTTAGGGACAGAGCCTAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTC 2895
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3002 CTGTTAGGGACAGAGCCTAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTC 3061

Qy       2896 ACAAACCCACGCTCACCTGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCAT 2955
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3062 ACAAACCCACGCTCACCTGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCAT 3121

Qy       2956 TAGGGGCCTTGCCAAGGTCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGG 3015
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3122 TAGGGGCCTTGCCAAGGTCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGG 3181

Qy       3016 GCTTTGACCACTACCATATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGC 3075
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3182 GCTTTGACCACTACCATATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGC 3241

Qy       3076 TAGTCACACTTTTCAGACCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGAT 3135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3242 TAGTCACACTTTTCAGACCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGAT 3301

Qy       3136 GGAGATAATTTTTTTTTCTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAG 3195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3302 GGAGATAATTTTTTTTTCTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAG 3361

Qy       3196 CTGAACCACCAGGAACCTGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGT 3255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3362 CTGAACCACCAGGAACCTGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGT 3421

Qy       3256 CTACCTCCCTCTTTGTAAATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATA 3315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3422 CTACCTCCCTCTTTGTAAATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATA 3481

Qy       3316 AAGATGAACTTGGTTTC 3332
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Db       3482 AAGATGAACTTGGTTTC 3498
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RESULT 5
US-10-343-357-17
; Sequence 17, Application US/10343357
; Publication No. US20040058341A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y.Tom
; APPLICANT: ELLIOTT, Vicki S.; RAMKUMAR, Jayalaxmi
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: LEE, Ernestine A.; HAFALIA, April J.A.

```
;  APPLICANT:  LU, Dyung Aina M.; TRIBOULEY, Catherine M.
;  APPLICANT:  GRIFFIN, Jennifer A.; BAUGHN, Mariah R.
;  APPLICANT:  YUE, Henry; WARREN, Bridget A.
;  APPLICANT:  NGUYEN, Danniel B.; CHAWLA, Narinder K.
;  APPLICANT:  KEARNEY, Liam
;  TITLE OF INVENTION: PROTEIN PHOSPHATASES
;  FILE REFERENCE: PI-0173 PCT
;  CURRENT APPLICATION NUMBER: US/10/343,357
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: PCT/US01/23716
;  PRIOR FILING DATE: 2001-07-26
;  PRIOR APPLICATION NUMBER: US 60/221,679
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: US 60/223,272
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: US 60/224,309
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US 60/226,728
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: US 60/229,254
;  PRIOR FILING DATE: 2000-08-30
;  PRIOR APPLICATION NUMBER: US 60/231,366
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PERL Program
; SEQ ID NO 17
;   LENGTH: 3766
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CB1
US-10-343-357-17

  Query Match             93.6%;  Score 3118.8;  DB 18;  Length 3766;
  Best Local Similarity   95.2%;  Pred. No. 0;
  Matches 3305;  Conservative    0;  Mismatches    2;  Indels  165;  Gaps    2;

Qy         25 GAAAAGAAGAGGAGGAGGAGAGCGACGGGACGGGACGCGAGCGGGAGCGCAGCCGCCCTC 84
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAAAGAAGATGAGGAGGAGAGCGACGGGACGGGACGCGAGCGGGAGCGCAGCCGCCCTC 60

Qy         85 TCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGCGAGGGGGGCCCGAGGGGAGACGCC 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGCGAGGGGGGCCCGAGGGGAGACGCC 120

Qy        145 GTGACAACTTTCGTTTCCCTCTGAGGGAATTGGGAGGTCGGCGGCCCCAAAAGCTTTCAG 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGACAACTTTCGTTTCCCTCTGAGGGAATTGGGAGGTCGGCGGCCCCAAAAGCTTTCAG 180

Qy        205 TCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATGCGCTGGCT 264
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Db        181 TCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATGCGCTGGCT 240

Qy        265 GCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGAATCAAATG 324
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Db        241 GCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGAATCAAATG 300

Qy        325 TGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAAGAGAAAGA 384
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Db        301 TGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAAGAGAAAGA 360

Qy        385 GACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCCAGTCACCA 444
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCCAGTCACCA 420

Qy        445 CCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGCACACCACC 504
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Qy        505 ATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTGTTGTCATG 564
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Db        481 ATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTGTTGTCATG 540

Qy        565 GCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGCTGGAAAGT 624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGCTGGAAAGT 600

Qy        625 GGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATACATCCCAC 684
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATACATCCCAC 660

Qy        685 ATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGCAACAGGAC 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGCAACAGGAC 720

Qy        745 AAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACATTGATTGC 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACATTGATTGC 780

Qy        805 AGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCTCTTCAGAC 864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCTCTTCAGAC 840

Qy        865 TGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTCACCTGCTT 924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTCACCTGCTT 900

Qy        925 GC---------------------------------------------------------- 926
              ||
Db        901 GCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAAAATCCACT 960

Qy        927 ---------------------------------------------------------- 926

Db        961 CTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGCCAACCCGA 1020

Qy        927 ----------------------------------------------AGGAGCTGATGCAG 940
                                                           ||||||||||||||
Db       1021 ATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGGAGCTGATGCAG 1080

Qy        941 CAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTTATC 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTTATC 1140

Qy       1001 CCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCG 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCG 1200

Qy       1061 TGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTA 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTA 1260

Qy       1121 GTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAG 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAG 1320

Qy       1181 AGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATA 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATA 1380

Qy       1241 TCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAACCAG 1300
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Db       1381 TCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAACCAG 1440

Qy       1301 ACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGCCAAATGAA 1360
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Db       1441 ACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGCCAAATGAA 1500

Qy       1361 CCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTCCACCCTGT 1420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTCCACCCTGT 1560

Qy       1421 GCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCAGCGTGCCC 1480
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Qy       1481 AGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTCAGT 1540
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Db       1621 AGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTCAGT 1680

Qy       1541 GGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCT 1600
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Db       1681 GGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCT 1740

Qy       1601 CTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATGGCTTCTCC 1660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATGGCTTCTCC 1800

Qy       1661 TCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGACCAACAAG 1720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGACCAACAAG 1860

Qy       1721 CTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCAGTCCTGAT 1780
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Db       1861 CTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCAGTCCTGAT 1920

Qy       1781 AAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACAGCCAGAGC 1840
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Db       1921 AAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACAGCCAGAGC 1980

Qy       1841 AAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCCTTTTATCT 1900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 AAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCCTTTTATCT 2040

Qy       1901 CCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTTTCGGCCTT 1960
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Db       2041 CCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTTTCGGCCTT 2100

Qy       1961 TCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCTGGCACTCG 2020
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Db       2101 TCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCTGGCACTCG 2160

Qy       2021 GATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATTTTGCCACA 2080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATTTTGCCACA 2220

Qy       2081 GAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTTACTCTGCC 2140
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Qy       2141 TACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCAGGCGGCAG 2200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCAGGCGGCAG 2340

Qy       2201 AAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCTTTGAAAAG 2260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2261 CAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAGAGAACAGG 2320
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Db       2401 CAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAGAGAACAGG 2460

Qy       2321 TCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAAATC 2380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 TCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAAATC 2520

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Db       2521 ATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTTTTTCTTGT 2580

Qy       2441 TCACAAAAAAATTCCCTGTAAATCTGAAATATATATATGTACATACATATATATTTTTGG 2500
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Qy       2501 AAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTCTCTTAACA 2560
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Qy       2561 TCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAGATGCTAGA 2620
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Db       2701 TCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAGATGCTAGG 2760

Qy       2621 ATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCTTGTTCTTA 2680
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Db       2761 ATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCTTGTTCTTA 2820

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Db       2821 AAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTT-CACGTTGTGCT 2879

Qy       2741 ACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCTTAGCGCTG 2800
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Db       2880 ACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCTTAGCGCTG 2939

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Qy       2861 AATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACCTGACAGCC 2920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3000 AATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACCTGACAGCC 3059

Qy       2921 GAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGGTCTACCTT 2980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3060 GAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGGTCTACCTT 3119

Qy       2981 AGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCATATCTGGTA 3040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3120 AGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCATATCTGGTA 3179

Qy       3041 GCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGACCAATTCA 3100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3180 GCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGACCAATTCA 3239

Qy       3101 AACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTTTCTTCTCAG 3160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3240 AACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTTTCTTCTCAG 3299

Qy       3161 CTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACCTGGCAACA 3220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3300 CTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACCTGGCAACA 3359

Qy       3221 TCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTAAATCAAAG 3280
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Db       3360 TCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTAAATCAAAG 3419

Qy       3281 AATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3332
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Db       3420 AATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3471
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RESULT 6
US-10-029-345A-108
; Sequence 108, Application US/10029345A
; Publication No. US20050130286A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
; FILE REFERENCE: D0072.NP
; CURRENT APPLICATION NUMBER: US/10/029,345A
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/256,868
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/280,186
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/287,735
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 60/295,848
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/300,465
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 208

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;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
;   LENGTH: 5450
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (538)..(2532)
US-10-029-345A-108

  Query Match            93.2%;  Score 3106.2;  DB 22;  Length 5450;
  Best Local Similarity  95.1%;  Pred. No. 0;
  Matches 3304;  Conservative    0;  Mismatches    3;  Indels  166;  Gaps    3;

Qy         25 GAAAAGAAGAGGAGGAGGAGAGCGACGGGACGGGACGCGAGCGGGAGCGCAGCCGCCCTC 84
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Qy         85 TCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGCGAGGGGGGCCCGAGGGGAGACGCC 144
Db         61 TCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGCGAGGGGGGCCCGAGGGGAGACGCC 120

Qy        145 GTGACAACTTTCGTTTCCCTCTGAGGGAATTGGGAGGTCGGCGGCCCCAAAAGCTTTCAG 204
Db        121 GTGACAACTTTCGTTTCCCTCTGAGGGAATTGGGAGGTCGGCGGCCCCAAAAGCTTTCAG 180

Qy        205 TCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATGCGCTGGCT 264
Db        181 TCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATGCGCTGGCT 240

Qy        265 GCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGAATCAAATG 324
Db        241 GCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGAATCAAATG 300

Qy        325 TGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAAGAGAAAGA 384
Db        301 TGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAAGAGAAAGA 360

Qy        385 GACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCCAGTCACCA 444
Db        361 GACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCCAGTCACCA 420

Qy        445 CCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGCACACCACC 504
Db        421 CCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGCACACCACC 480

Qy        505 ATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTGTTGTCATG 564
Db        481 ATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTGTTGTCATG 540

Qy        565 GCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGCTGGAAAGT 624
Db        541 GCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGCTGGAAAGT 600

Qy        625 GGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATACATCCCAC 684
Db        601 GGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATACATCCCAC 660

Qy        685 ATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGCAACAGGAC 744
Db        661 ATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGCAACAGGAC 720

Qy        745 AAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACATTGATTGC 804
Db        721 AAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACATTGATTGC 780

Qy        805 AGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCTCTTCAGAC 864
Db        781 AGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCTCTTCAGAC 840

Qy        865 TGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTCACCTGCTT 924
Db        841 TGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTCACCTGCTT 900

Qy        925 GC---------------------------------------------------------- 926
              ||
Db        901 GCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAAAATCCACT 960

Qy        927 ---------------------------------------------------------- 926

Db        961 CTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGCCAACCCGA 1020

Qy        927 ----------------------------------------------AGGAGCTGATGCAG 940
                                                           ||||||||||  |||
Db       1021 ATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGGAGCTGATACAG 1080

Qy        941 CAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTTATC 1000
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1081 CAGAATGGGATTGGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCCTGACTTTATC 1140

Qy       1001 CCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCG 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCG 1200

Qy       1061 TGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTA 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGATGTGTTCTA 1260

Qy       1121 GTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAG 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAG 1320

Qy       1181 AGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATA 1240
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Db       1321 AGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATA 1380

Qy       1241 TCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAACCAG 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAACCAG 1440

Qy       1301 ACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGCCAAATGAA 1360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGCCAAATGAA 1500

Qy       1361 CCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTCCACCCTGT 1420
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Db       1501 CCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTCCACCCTGT 1560

Qy       1421 GCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCAGCGTGCCC 1480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCAGCGTGCCC 1620

Qy       1481 AGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTCAGT 1540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTCAGT 1680

Qy       1541 GGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCT 1600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCT 1740

Qy       1601 CTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATGGCTTCTCC 1660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATGGCTTCTCC 1800

Qy       1661 TCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGACCAACAAG 1720
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Db       1801 TCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGACCAACAAG 1860

Qy       1721 CTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCAGTCCTGAT 1780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCAGTCCTGAT 1920

Qy       1781 AAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACAGCCAGAGC 1840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACAGCCAGAGC 1980
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Qy       1841 AAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCCTTTTATCT 1900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 AAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCCTTTTATCT 2040

Qy       1901 CCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTTTCGGCCTT 1960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTTTCGGCCTT 2100

Qy       1961 TCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCTGGCACTCG 2020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCTGGCACTCG 2160

Qy       2021 GATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATTTTGCCACA 2080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATTTTGCCACA 2220

Qy       2081 GAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTTACTCTGCC 2140
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Db       2221 GAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTTACTCTGCC 2280

Qy       2141 TACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCAGGCGGCAG 2200
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Db       2281 TACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCAGGCGGCAG 2340

Qy       2201 AAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCTTTGAAAAG 2260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCTTTGAAAAG 2400

Qy       2261 CAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAGAGAACAGG 2320
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Db       2401 CAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAGAGAACAGG 2460

Qy       2321 TCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAAATC 2380
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Db       2461 TCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAAATC 2520

Qy       2381 ATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAA-TTTTTTTTTCTTG 2439
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Db       2521 ATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTTTTTTCTTG 2580

Qy       2440 TTCACAAAAAAATTCCCTGTAAATCTGAAATATATATATGTACATACATATATATTTTTG 2499
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Db       2581 TTCACAAAAAAATTCCCTGTAAATCTGAAATATATATATGTACATACATATATATTTTTG 2640

Qy       2500 GAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTCTCTTAAC 2559
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Qy       2560 ATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAGATGCTAG 2619
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Db       2701 ATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAGATGCTAG 2760

Qy       2620 AATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCTTGTTCTT 2679
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Db       2761 AATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCTTGTTCTT 2820

Qy       2680 AAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTTCCACGTTGTGC 2739
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Db       2821 AAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTT-CACGTTGTGC 2879

Qy       2740 TACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCTTAGCGCT 2799
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Db       2880 TACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCTTAGCGCT 2939

Qy       2800 GAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCCTAGTGGT 2859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2940 GAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCCTAGTGGT 2999

Qy       2860 AAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACCTGACAGC 2919
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Db       3000 AAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACCTGACAGC 3059

Qy       2920 CGAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGGTCTACCT 2979
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Db       3060 CGAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGGTCTACCT 3119

Qy       2980 TAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCATATCTGGT 3039
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3120 TAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCATATCTGGT 3179

Qy       3040 AGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGACCAATTC 3099
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Db       3180 AGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGACCAATTC 3239

Qy       3100 AAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTTCTTCTCA 3159
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Db       3240 AAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTTCTTCTCA 3299

Qy       3160 GCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACCTGGCAAC 3219
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Db       3300 GCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACCTGGCAAC 3359

Qy       3220 ATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTAAATCAAA 3279
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Db       3360 ATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTAAATCAAA 3419

Qy       3280 GAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3332
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RESULT 7
US-10-029-345A-147
; Sequence 147, Application US/10029345A
; Publication No. US20050130286A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
; FILE REFERENCE: D0072.NP
; CURRENT APPLICATION NUMBER: US/10/029,345A
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/256,868
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/280,186
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/287,735
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 60/295,848
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/300,465
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 147
; LENGTH: 5450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (538)..(2532)
US-10-029-345A-147

Query Match 93.2%; Score 3106.2; DB 22; Length 5450;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 3304; Conservative 0; Mismatches 3; Indels 166; Gaps 3;

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Db          1 GAAAAGAAGACGAGGAGGAGAGCGACGGGACGGGACGCGAGCGGGAGCGCAGCCGCCCTC 60

Qy         85 TCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGCGAGGGGGGCCCGAGGGGAGACGCC 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGCGAGGGGGGCCCGAGGGGAGACGCC 120

Qy        145 GTGACAACTTTCGTTTCCCTCTGAGGGAATTGGGAGGTCGGCGGCCCCAAAAGCTTTCAG 204
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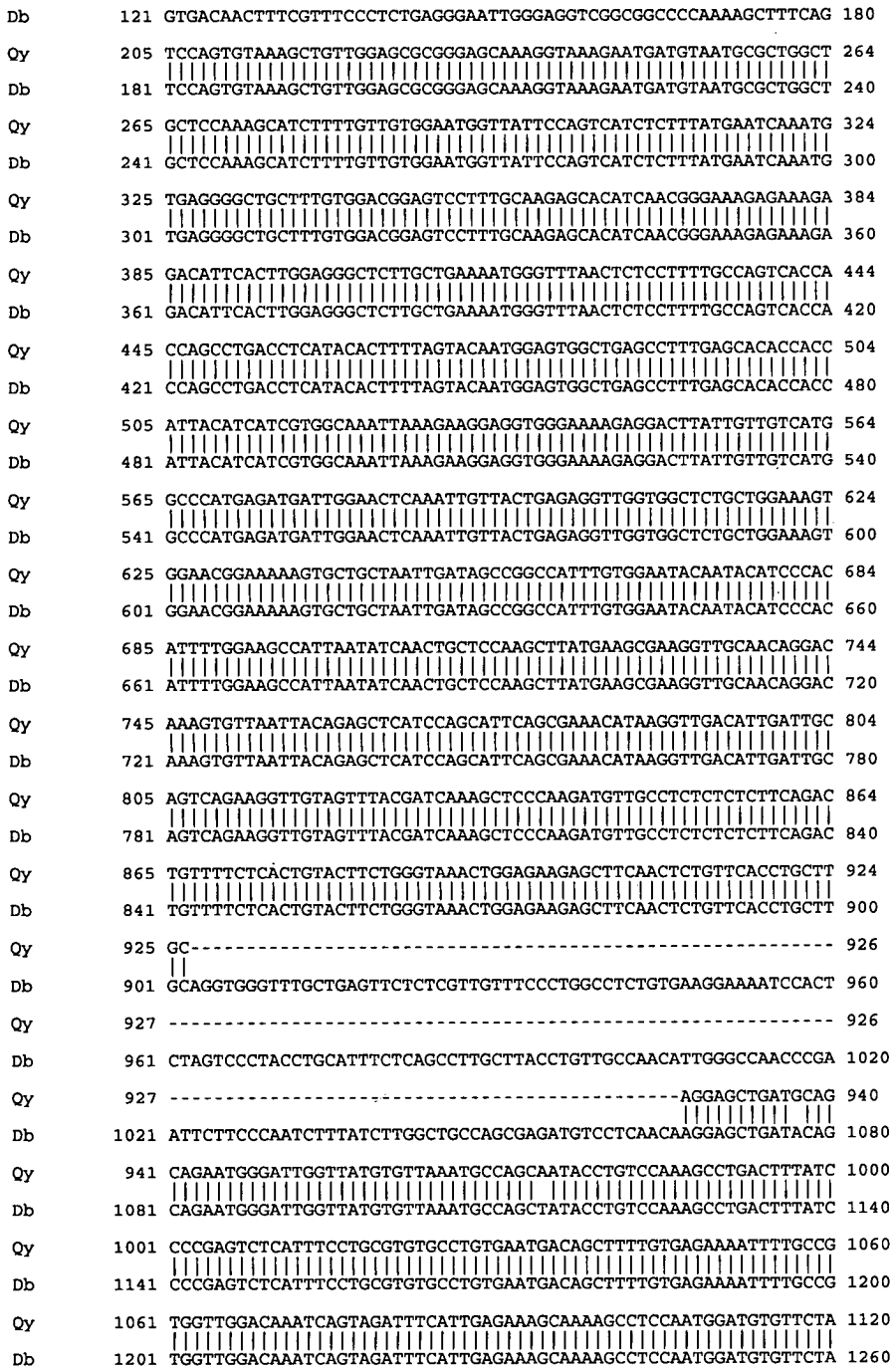
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Qy 205 TCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATGCGCTGGCT 264
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Qy 325 TGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAAGAGAAAGA 384
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Qy 445 CCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGCACACCACC 504
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Qy 505 ATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTGTTGTCATG 564
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Qy 625 GGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATACATCCCAC 684
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Qy 927 ---------- 926
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RESULT 8
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2583)
US-09-816-494-1

Query Match 88.5%; Score 2950; DB 9; Length 3544;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;

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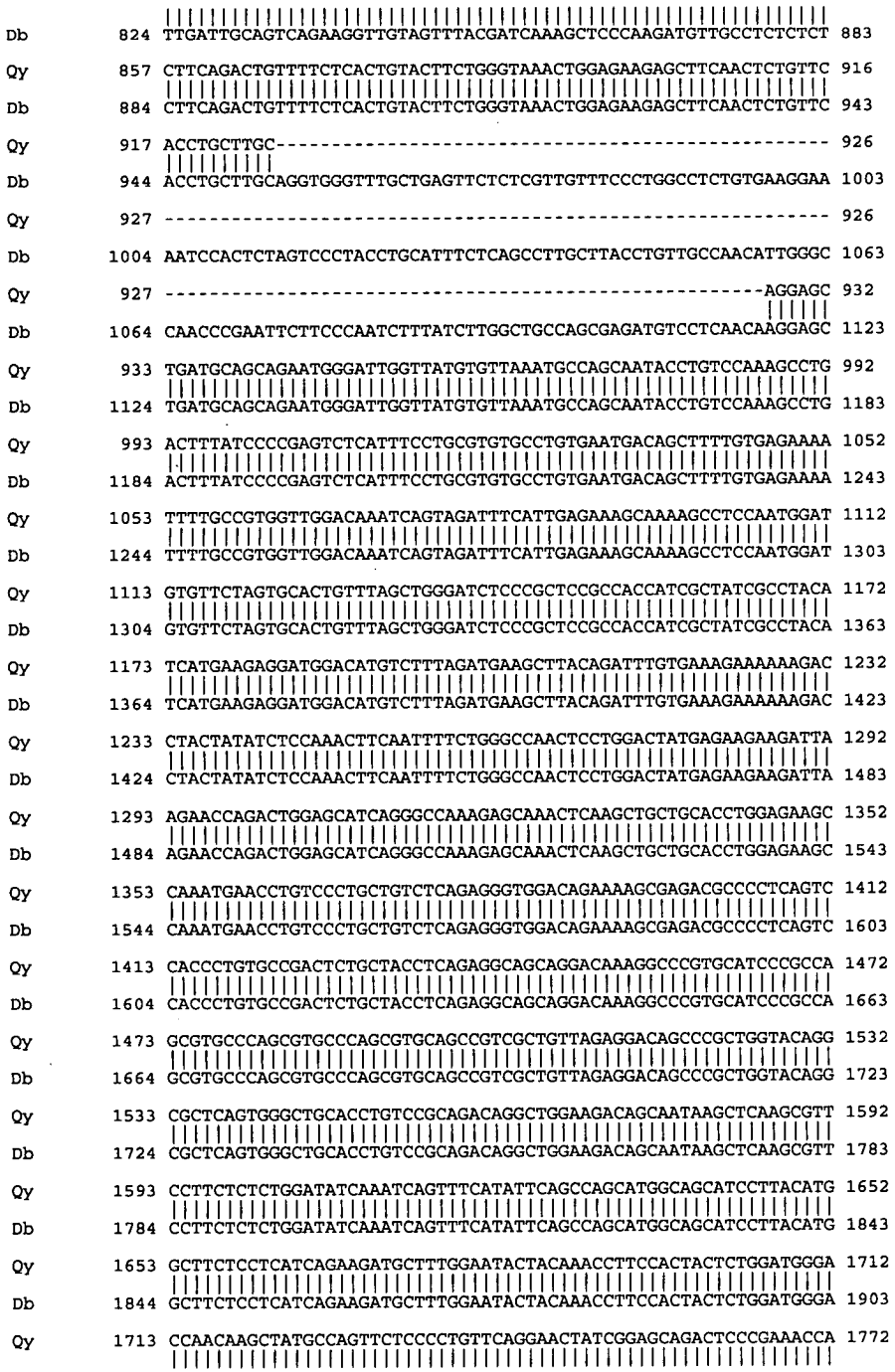
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Qy       2973 TCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3163 TCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3222

Qy       3033 ATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGA 3092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3223 ATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGA 3282

Qy       3093 CCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTT 3152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3283 CCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTT 3342

Qy       3153 CTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACC 3212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3343 CTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACC 3402

Qy       3213 TGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3403 TGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3462

Qy       3273 AATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3463 AATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3522
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RESULT 9
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040009501A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals Inc.
;  APPLICANT:  Curtis, Rory A.J.
;  APPLICANT:  Logan, Thomas Joseph
;  APPLICANT:  Glucksmann, Maria A.
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  Williamson, Mark J.
;  APPLICANT:  Rudolph-Owen, Laura A.
;  APPLICANT:  Chun, Miyoung
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
;  TITLE OF INVENTION:  38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: MPI03-018OMNIM
;  CURRENT APPLICATION NUMBER: US/10/377,072
;  CURRENT FILING DATE:  2003-02-27
;  PRIOR APPLICATION NUMBER: US 09/895,860
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/215,370
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: US 09/723,806
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: US 60/187,455
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 09/843,297
;  PRIOR FILING DATE: 2001-04-25
;  PRIOR APPLICATION NUMBER: US 60/199,801
;  PRIOR FILING DATE: 2000-04-26
;  PRIOR APPLICATION NUMBER: US 09/861,801
;  PRIOR FILING DATE: 2001-05-21
;  PRIOR APPLICATION NUMBER: US 60/205,508
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 09/816,494
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: US 09/815,419
;  PRIOR FILING DATE: 2001-03-22
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 3544
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (589)...(2586)
US-10-377-072-25

  Query Match            88.5%;  Score 2950;  DB 17;  Length 3544;
  Best Local Similarity  95.0%;  Pred. No. 0;
  Matches 3135;  Conservative    0;  Mismatches    0;  Indels  165;  Gaps    2;
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Qy        197 GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATG 256
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Db        224 GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATG 283

Qy        257 CGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGA 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 CGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGA 343

Qy        317 ATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAA 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 ATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAA 403

Qy        377 GAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCC 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCC 463

Qy        437 AGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGC 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 AGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGC 523

Qy        497 ACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTG 556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 ACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTG 583

Qy        557 TTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGC 616
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Db        584 TTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGC 643

Qy        617 TGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATA 676
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Db        644 TGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATA 703

Qy        677 CATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGC 736
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Db        704 CATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGC 763

Qy        737 AACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACA 796
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 AACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACA 823

Qy        797 TTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCT 856
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Db        824 TTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCT 883

Qy        857 CTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTC 916
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 CTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTC 943

Qy        917 ACCTGCTTGC---------------------------------------------------- 926
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Db        944 ACCTGCTTGCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAA 1003

Qy        927 ---------------------------------------------------------- 926

Db       1004 AATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGC 1063
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Qy       927 ----------------------------------------------------------AGGAGC 932
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Db      1064 CAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGGAGC 1123

Qy       933 TGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTG 992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1124 TGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTG 1183

Qy       993 ACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAA 1052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1184 ACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAA 1243

Qy      1053 TTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGAT 1112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1244 TTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGAT 1303

Qy      1113 GTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACA 1172
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Db      1304 GTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACA 1363

Qy      1173 TCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGAC 1232
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Db      1364 TCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGAC 1423

Qy      1233 CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTA 1292
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Db      1424 CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTA 1483

Qy      1293 AGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGC 1352
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Db      1484 AGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGC 1543

Qy      1353 CAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTC 1412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1544 CAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTC 1603

Qy      1413 CACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCA 1472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1604 CACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCA 1663

Qy      1473 GCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG 1532
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Db      1664 GCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG 1723

Qy      1533 CGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1592
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Db      1724 CGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1783

Qy      1593 CCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATG 1652
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Db      1784 CCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATG 1843

Qy      1653 GCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGA 1712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1844 GCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGA 1903

Qy      1713 CCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCA 1772
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Db      1904 CCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCA 1963

Qy      1773 GTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACA 1832
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Db      1964 GTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACA 2023

Qy      1833 GCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCC 1892
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Db      2024 GCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCC 2083

Qy      1893 TTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTT 1952
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Db      2084 TTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTT 2143

Qy      1953 TCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCT 2012
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Db      2144 TCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCT 2203

Qy      2013 GGCACTCGGATATCTTGGCCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATT 2072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2204 GGCACTCGGATATCTTGGCCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATT 2263

Qy      2073 TTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTT 2132
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Db      2264 TTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTT 2323

Qy      2133 ACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCA 2192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2324 ACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCA 2383

Qy      2193 GGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCT 2252
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Db      2384 GGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCT 2443

Qy      2253 TTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAG 2312
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Db      2444 TTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAG 2503

Qy      2313 AGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCA 2372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2504 AGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCA 2563

Qy      2373 TGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTT 2432
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Db      2564 TGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTT 2623

Qy      2433 TTTCTTGTTCACAAAAAAAATTCCCTGTAAATCTGAAATATATATATGTACATACATATAT 2492
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Qy      2493 ATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTC 2552
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Qy      2553 TCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAG 2612
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Qy      2613 ATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCT 2672
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Qy      2673 TGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTTCCAC 2732
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Db      2864 TGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTT-CAC 2922

Qy      2733 GTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCT 2792
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Db      2923 GTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCT 2982

Qy      2793 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCC 2852
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Db      2983 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCC 3042

Qy      2853 TAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACC 2912
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Db      3043 TAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACC 3102

Qy      2913 TGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGG 2972
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Db      3103 TGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGG 3162

Qy      2973 TCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3163 TCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3222

Qy      3033 ATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGA 3092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3223 ATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGA 3282

Qy       3093 CCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTT 3152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3283 CCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTT 3342

Qy       3153 CTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACC 3212
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Db       3343 CTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACC 3402

Qy       3213 TGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3403 TGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3462

Qy       3273 AATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3463 AATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3522
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RESULT 10
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040157221A9
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals Inc.
;  APPLICANT:  Curtis, Rory A.J.
;  APPLICANT:  Logan, Thomas Joseph
;  APPLICANT:  Glucksmann, Maria A.
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  Williamson, Mark J.
;  APPLICANT:  Rudolph-Owen, Laura A.
;  APPLICANT:  Chun, Miyoung
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
;  TITLE OF INVENTION:  38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: MPI03-018OMNIM
;  CURRENT APPLICATION NUMBER: US/10/377,072
;  CURRENT FILING DATE:  2003-02-27
;  PRIOR APPLICATION NUMBER: US 09/895,860
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/215,370
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: US 09/723,806
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: US 60/187,455
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 09/843,297
;  PRIOR FILING DATE: 2001-04-25
;  PRIOR APPLICATION NUMBER: US 60/199,801
;  PRIOR FILING DATE: 2000-04-26
;  PRIOR APPLICATION NUMBER: US 09/861,801
;  PRIOR FILING DATE: 2001-05-21
;  PRIOR APPLICATION NUMBER: US 60/205,508
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 09/816,494
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: US 09/815,419
;  PRIOR FILING DATE: 2001-03-22
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 3544
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (589)...(2586)
US-10-377-072-25

  Query Match             88.5%;  Score 2950;  DB 19;  Length 3544;
  Best Local Similarity   95.0%;  Pred. No. 0;
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Qy        197 GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATG 256
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Db        224 GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATG 283

Qy        257 CGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGA 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 CGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGA 343

Qy        317 ATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAA 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 ATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAA 403

Qy        377 GAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCC 436
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Db        404 GAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCC 463

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Qy        497 ACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTG 556
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Db        524 ACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTG 583

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Qy        617 TGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATA 676
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Qy        677 CATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGC 736
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Qy        917 ACCTGCTTGC---------------------------------------------------- 926
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Qy        927 ---------------------------------------------------------- 926

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Qy        927 ----------------------------------------------------------AGGAGC 932
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Qy        933 TGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTG 992
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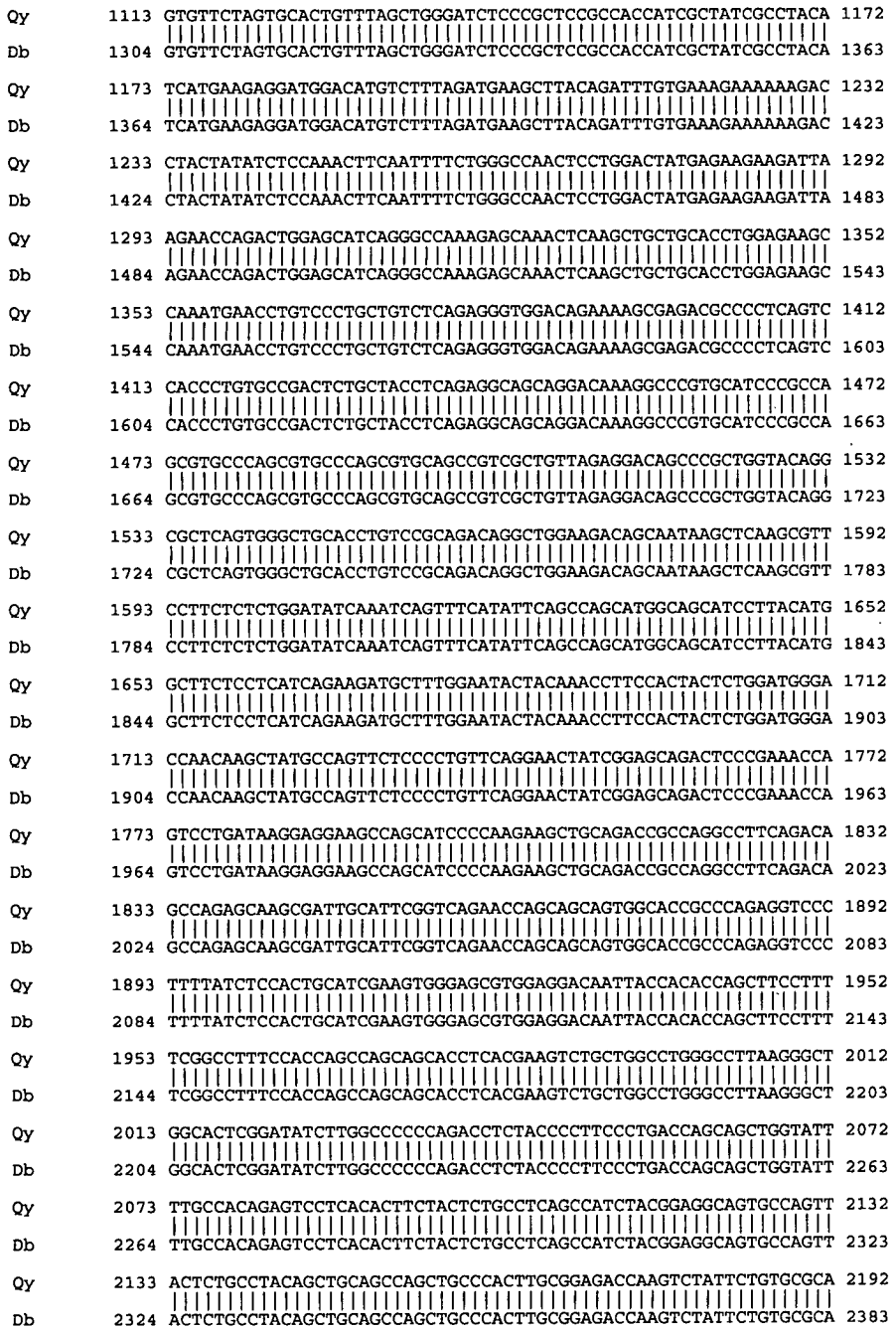
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Db 1604 CACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCA 1663
Qy 1473 GCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG 1532
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Qy 2553 TCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAG 2612
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RESULT 11
US-10-357-930-20824
; Sequence 20824, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20824
;   LENGTH: 5145
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
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;   OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20824

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Qy        917 ACCTGCTTGC---------------------------------------------------- 926
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Qy        927 ---------------------------------------------------------- 926

Db       1004 AATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGC 1063

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                                                                   ||||||
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Db       1424 CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTA 1483

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1544 CAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTC 1603

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Qy       1473 GCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG 1532
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Qy       1533 CGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1592
Db       1724 CGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1783
Qy       1593 CCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATG 1652
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Qy       1953 TCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCT 2012
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Db       2204 GGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATT 2263
Qy       2073 TTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTT 2132
Db       2264 TTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTT 2323
Qy       2133 ACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCA 2192
Db       2324 ACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCA 2383
Qy       2193 GGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCT 2252
Db       2384 GGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCT 2443
Qy       2253 TTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAG 2312
Db       2444 TTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAG 2503
Qy       2313 AGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCA 2372
Db       2504 AGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCA 2563
Qy       2373 TGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTT 2432
Db       2564 TGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTT 2623
Qy       2433 TTTCTTGTTCACAAAAAAATTCCCTGTAAATCTGAAATATATATATGTACATACATATAT 2492
Db       2624 TTTCTTGTTCACAAAAAAATTCCCTGTAAATCTGAAATATATATATGTACATACATATAT 2683
Qy       2493 ATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTC 2552
Db       2684 ATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTC 2743
Qy       2553 TCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAG 2612
Db       2744 TCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAG 2803
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Qy       2613 ATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCT 2672
Db       2804 ATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCT 2863
Qy       2673 TGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTTCCAC 2732
Db       2864 TGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTT-CAC 2922
Qy       2733 GTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCT 2792
Db       2923 GTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCT 2982
Qy       2793 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCC 2852
Db       2983 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCC 3042
Qy       2853 TAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACC 2912
Db       3043 TAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACC 3102
Qy       2913 TGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGG 2972
Db       3103 TGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGG 3162
Qy       2973 TCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3032
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Qy       3033 ATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGA 3092
Db       3223 ATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGA 3282
Qy       3093 CCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTT 3152
Db       3283 CCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTT 3342
Qy       3153 CTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACC 3212
Db       3343 CTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACC 3402
Qy       3213 TGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3272
Db       3403 TGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3462
Qy       3273 AATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3332
Db       3463 AATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3522
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US-10-357-930-20969
; Sequence 20969, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
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;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20969
;   LENGTH: 5145
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 5144, 5145
;   OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20969

  Query Match             88.5%;  Score 2950;  DB 20;  Length 5145;
  Best Local Similarity   95.0%;  Pred. No. 0;
  Matches 3135;  Conservative    0;  Mismatches    0;  Indels  165;  Gaps    2;

Qy        197 GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATG 283

Qy        257 CGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGA 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 CGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGA 343

Qy        317 ATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAA 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 ATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAA 403

Qy        377 GAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCC 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCC 463

Qy        437 AGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGC 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 AGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGC 523

Qy        497 ACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTG 556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 ACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTG 583

Qy        557 TTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGC 616
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 TTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGC 643

Qy        617 TGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATA 676
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 TGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATA 703

Qy        677 CATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGC 736
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 CATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGC 763

Qy        737 AACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACA 796
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 AACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACA 823

Qy        797 TTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCT 856
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 TTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCT 883

Qy        857 CTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTC 916
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 CTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTC 943

Qy        917 ACCTGCTTGC---------------------------------------------------- 926
              ||||||||||
Db        944 ACCTGCTTGCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAA 1003

Qy        927 ---------------------------------------------------------- 926

Db       1004 AATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGC 1063

Qy        927 ----------------------------------------------------------AGGAGC 932
                                                                           ||||||
Db       1064 CAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGGAGC 1123

Qy        933 TGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTG 992
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 TGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTG 1183

Qy        993 ACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAA 1052
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 ACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAA 1243

Qy       1053 TTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGAT 1112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 TTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGAT 1303

Qy       1113 GTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACA 1172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 GTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACA 1363

Qy       1173 TCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGAC 1232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1364 TCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGAC 1423

Qy       1233 CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTA 1292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1424 CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTA 1483

Qy       1293 AGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGC 1352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1484 AGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGC 1543

Qy       1353 CAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTC 1412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1544 CAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTC 1603

Qy       1413 CACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCA 1472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1604 CACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCA 1663

Qy       1473 GCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG 1532
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Db       1664 GCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG 1723

Qy       1533 CGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1724 CGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1783

Qy       1593 CCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATG 1652
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1784 CCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATG 1843

Qy       1653 GCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGA 1712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1844 GCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGA 1903

Qy       1713 CCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCA 1772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1904 CCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCA 1963

Qy       1773 GTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACA 1832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1964 GTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACA 2023

Qy       1833 GCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCC 1892
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2024 GCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCC 2083

Qy       1893 TTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTT 1952
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Db       2084 TTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTT 2143
Qy       1953 TCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCT 2012
Db       2144 TCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCT 2203
Qy       2013 GGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATT 2072
Db       2204 GGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATT 2263
Qy       2073 TTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTT 2132
Db       2264 TTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTT 2323
Qy       2133 ACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCA 2192
Db       2324 ACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCA 2383
Qy       2193 GGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCT 2252
Db       2384 GGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCT 2443
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Db       2444 TTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAG 2503
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Qy       2373 TGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTT 2432
Db       2564 TGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTT 2623
Qy       2433 TTTCTTGTTCACAAAAAAATTCCCTGTAAATCTGAAATATATATATGTACATACATATAT 2492
Db       2624 TTTCTTGTTCACAAAAAAATTCCCTGTAAATCTGAAATATATATATGTACATACATATAT 2683
Qy       2493 ATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTC 2552
Db       2684 ATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTC 2743
Qy       2553 TCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAG 2612
Db       2744 TCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAG 2803
Qy       2613 ATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCT 2672
Db       2804 ATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCT 2863
Qy       2673 TGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTTCCAC 2732
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Qy       2733 GTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCT 2792
Db       2923 GTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCT 2982
Qy       2793 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCC 2852
Db       2983 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCC 3042
Qy       2853 TAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACC 2912
Db       3043 TAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACC 3102
Qy       2913 TGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGG 2972
Db       3103 TGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGG 3162
Qy       2973 TCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3032
Db       3163 TCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3222
Qy       3033 ATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGA 3092
Db       3223 ATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGA 3282
Qy       3093 CCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTT 3152
Db       3283 CCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTT 3342
Qy       3153 CTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACC 3212
Db       3343 CTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACC 3402
Qy       3213 TGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3272
Db       3403 TGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3462
Qy       3273 AATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3332
Db       3463 AATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3522
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RESULT 13
US-10-357-930-21071
; Sequence 21071, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21071
;   LENGTH: 5145
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 5144, 5145
;   OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21071

  Query Match            88.5%;  Score 2950;  DB 20;  Length 5145;
  Best Local Similarity  95.0%;  Pred. No. 0;
  Matches 3135;  Conservative    0;  Mismatches    0;  Indels  165;  Gaps    2;

Qy        197 GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATG 256
Db        224 GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATG 283

Qy        257 CGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGA 316
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Db        284 CGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGA 343

Qy        317 ATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAA 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 ATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAA 403

Qy        377 GAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCC 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCC 463

Qy        437 AGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGC 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 AGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGC 523

Qy        497 ACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTG 556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 ACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTG 583

Qy        557 TTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGC 616
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 TTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGC 643

Qy        617 TGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATA 676
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 TGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATA 703

Qy        677 CATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGC 736
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 CATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGC 763

Qy        737 AACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACA 796
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 AACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACA 823

Qy        797 TTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCT 856
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 TTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCT 883

Qy        857 CTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTC 916
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 CTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTC 943

Qy        917 ACCTGCTTGC---------------------------------------------------- 926
              ||||||||||
Db        944 ACCTGCTTGCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAA 1003

Qy        927 ---------------------------------------------------------- 926

Db       1004 AATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGC 1063

Qy        927 ----------------------------------------------------------AGGAGC 932
                                                                         ||||||
Db       1064 CAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGGAGC 1123

Qy        933 TGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTG 992
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 TGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTG 1183

Qy        993 ACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAA 1052
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 ACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAA 1243

Qy       1053 TTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGAT 1112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 TTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGAT 1303

Qy       1113 GTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACA 1172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 GTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACA 1363

Qy       1173 TCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGAC 1232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1364 TCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGAC 1423

Qy       1233 CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTA 1292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1293 AGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGC 1352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1484 AGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGC 1543

Qy       1353 CAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTC 1412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1544 CAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTC 1603

Qy       1413 CACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCA 1472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1604 CACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCA 1663

Qy       1473 GCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG 1532
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1664 GCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG 1723

Qy       1533 CGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1593 CCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATG 1652
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1653 GCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGA 1712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1844 GCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGA 1903

Qy       1713 CCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCA 1772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1904 CCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCA 1963

Qy       1773 GTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACA 1832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1964 GTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACA 2023

Qy       1833 GCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCC 1892
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Db       2024 GCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCC 2083

Qy       1893 TTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTT 1952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2084 TTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTT 2143

Qy       1953 TCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCT 2012
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Db       2144 TCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCT 2203

Qy       2013 GGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATT 2072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2204 GGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATT 2263

Qy       2073 TTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTT 2132
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Db       2264 TTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTT 2323

Qy       2133 ACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCA 2192
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Db       2324 ACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCA 2383

Qy       2193 GGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCT 2252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2384 GGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCT 2443

Qy       2253 TTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAG 2312
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Db       2444 TTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAG 2503
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Qy       2313 AGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCA 2372
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Db       2504 AGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCA 2563

Qy       2373 TGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTTT 2432
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Db       2564 TGGAAATCATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTTT 2623

Qy       2433 TTTCTTGTTCACAAAAAAATTCCCTGTAAATCTGAAATATATATATGTACATACATATAT 2492
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Db       2624 TTTCTTGTTCACAAAAAAATTCCCTGTAAATCTGAAATATATATATGTACATACATATAT 2683

Qy       2493 ATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTC 2552
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Db       2684 ATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTC 2743

Qy       2553 TCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAG 2612
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Db       2744 TCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAG 2803

Qy       2613 ATGCTAGAATCCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCT 2672
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Qy       2673 TGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTTCCAC 2732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       2864 TGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTT-CAC 2922

Qy       2733 GTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCT 2792
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Qy       2793 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCC 2852
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Db       2983 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCC 3042

Qy       2853 TAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACC 2912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3043 TAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACC 3102

Qy       2913 TGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGG 2972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3103 TGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGG 3162

Qy       2973 TCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3163 TCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3222

Qy       3033 ATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGA 3092
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Db       3223 ATCTGGTAGCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGA 3282

Qy       3093 CCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTT 3152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3283 CCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTT 3342

Qy       3153 CTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACC 3212
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Db       3343 CTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACC 3402

Qy       3213 TGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3272
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Db       3403 TGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3462

Qy       3273 AATCAAAGAATTGTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTC 3332
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RESULT 14
US-10-357-930-21083
; Sequence 21083, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21083
;   LENGTH: 5145
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 5144, 5145
;   OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21083

  Query Match             88.5%;  Score 2950;  DB 20;  Length 5145;
  Best Local Similarity   95.0%;  Pred. No. 0;
  Matches 3135;  Conservative    0;  Mismatches    0;  Indels  165;  Gaps    2;

Qy        197 GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATG 256
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Qy        257 CGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGA 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 CGCTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATTCCAGTCATCTCTTTATGA 343

Qy        317 ATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAA 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 ATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAA 403

Qy        377 GAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCC 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCC 463

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Db        464 AGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGC 523

Qy        497 ACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTG 556
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Db        524 ACACCACCATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTG 583

Qy        557 TTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGC 616
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 TTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTGAGAGGTTGGTGGCTCTGC 643

Qy        617 TGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATA 676
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 TGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACAATA 703

Qy        677 CATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGC 736
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Db        704 CATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGC 763
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Db        764 AACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACA 823
Qy        797 TTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCT 856
Db        824 TTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCT 883
Qy        857 CTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTC 916
Db        884 CTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTC 943
Qy        917 ACCTGCTTGC---------------------------------------------------- 926
Db        944 ACCTGCTTGCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAA 1003
Qy        927 ---------------------------------------------------------- 926
Db       1004 AATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGC 1063
Qy        927 ----------------------------------------------------------AGGAGC 932
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Qy        993 ACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAA 1052
Db       1184 ACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAA 1243
Qy       1053 TTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGAT 1112
Db       1244 TTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATGGAT 1303
Qy       1113 GTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACA 1172
Db       1304 GTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACA 1363
Qy       1173 TCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGAC 1232
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Qy       1233 CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTA 1292
Db       1424 CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTA 1483
Qy       1293 AGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGC 1352
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Qy       1353 CAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCAGTC 1412
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Qy       1413 CACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCA 1472
Db       1604 CACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCA 1663
Qy       1473 GCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG 1532
Db       1664 GCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG 1723
Qy       1533 CGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1592
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Qy       1593 CCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATG 1652
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Qy       1653 GCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGA 1712
Db       1844 GCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGA 1903
Qy       1713 CCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCA 1772
Db       1904 CCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCA 1963
Qy       1773 GTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACA 1832
Db       1964 GTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACA 2023
Qy       1833 GCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCC 1892
Db       2024 GCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGCACCGCCCAGAGGTCCC 2083
Qy       1893 TTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTT 1952
Db       2084 TTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTT 2143
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Db       2144 TCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCT 2203
Qy       2013 GGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATT 2072
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Qy       2613 ATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCT 2672
Db       2804 ATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCT 2863
Qy       2673 TGTTCTTAAAAAAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTTCCAC 2732
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Qy       2733 GTTGTGCTACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCT 2792
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Qy       2973 TCTACCTTAGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3032
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; Publication No. US20040259086A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
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;   LENGTH: 5145
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 5144, 5145
;   OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21303

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Qy        317 ATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAA 376
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Qy        377 GAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCC 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        437 AGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGC 496
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Qy        677 CATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGC 736
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Qy        927 ---------------------------------------------------------- 926

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Qy        927 ----------------------------------------------------AGGAGC 932
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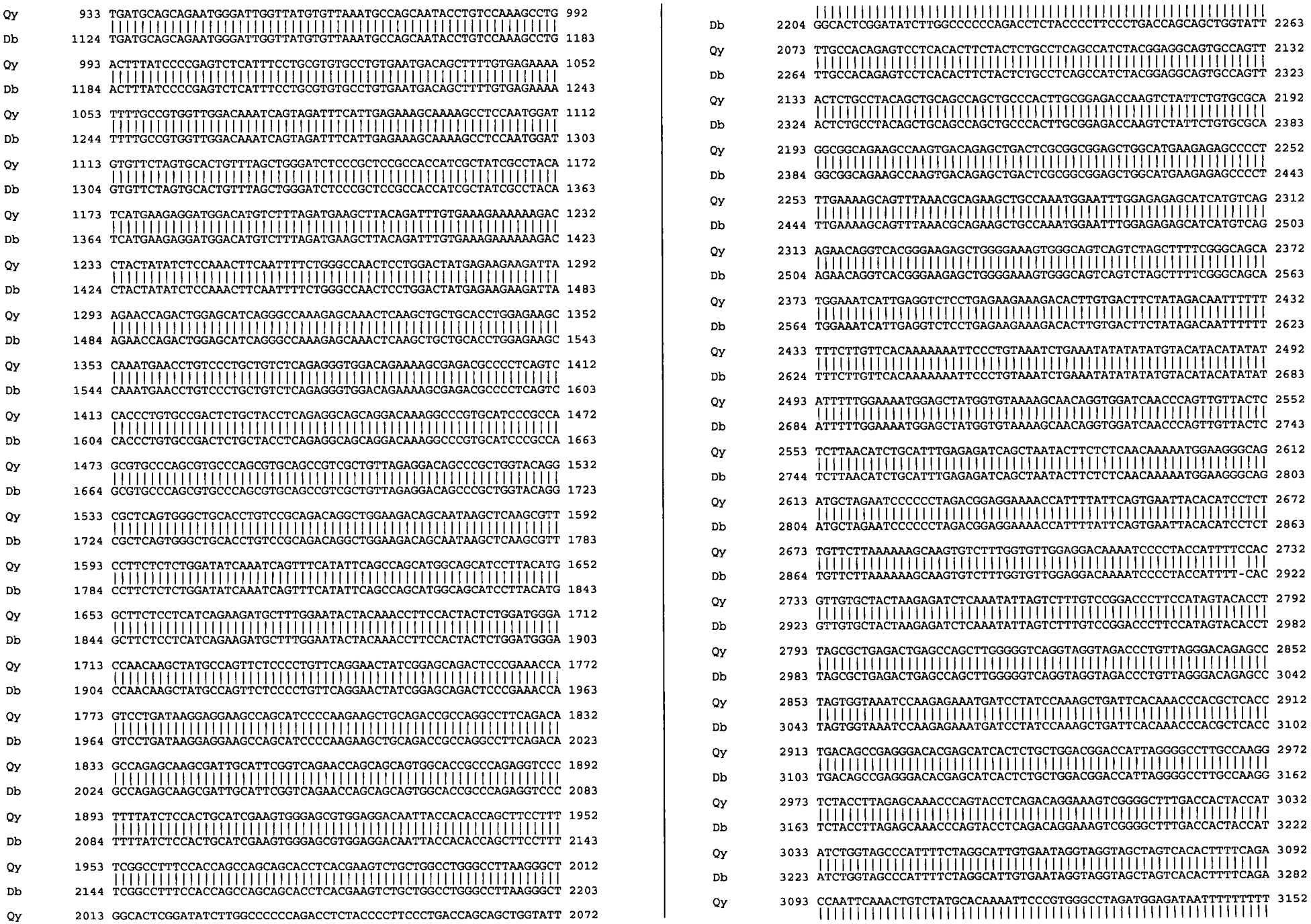
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Search completed: September 1, 2005, 11:36:52
Job time : 2092 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 1, 2005, 11:02:30 ; Search time 957 Seconds
(without alignments)
3537.918 Million cell updates/sec

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Perfect score: 2668
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2668	100.0	3332	9	US-09-964-277-20	Sequence 20, Appl
2	2606	97.7	1998	9	US-09-816-494-3	Sequence 3, Appli
3	2606	97.7	1998	17	US-10-377-072-27	Sequence 27, Appl
4	2606	97.7	1998	19	US-10-377-072-27	Sequence 27, Appl
5	2606	97.7	2102	17	US-10-094-749-673	Sequence 673, App
6	2606	97.7	2732	18	US-10-168-506-2	Sequence 2, Appli
7	2606	97.7	2732	21	US-10-838-181-2	Sequence 2, Appli
8	2606	97.7	2966	18	US-10-296-115-520	Sequence 520, App
9	2606	97.7	3059	18	US-10-257-026-1	Sequence 1, Appli
10	2606	97.7	3496	9	US-09-964-277-1	Sequence 1, Appli
11	2606	97.7	3521	20	US-10-370-715B-261	Sequence 261, App
12	2606	97.7	3544	9	US-09-816-494-1	Sequence 1, Appli
13	2606	97.7	3544	17	US-10-377-072-25	Sequence 25, Appl
14	2606	97.7	3544	19	US-10-377-072-25	Sequence 25, Appl
15	2606	97.7	3625	18	US-10-425-114-26234	Sequence 26234, A
16	2606	97.7	3766	18	US-10-343-357-17	Sequence 17, Appl
17	2606	97.7	4790	19	US-10-648-593-115	Sequence 115, App
18	2606	97.7	5145	20	US-10-357-930-20824	Sequence 20824, A
19	2606	97.7	5145	20	US-10-357-930-20969	Sequence 20969, A
20	2606	97.7	5145	20	US-10-357-930-21071	Sequence 21071, A
21	2606	97.7	5145	20	US-10-357-930-21083	Sequence 21083, A
22	2606	97.7	5145	20	US-10-357-930-21303	Sequence 21303, A
23	2606	97.7	5145	20	US-10-357-930-21307	Sequence 21307, A
24	2606	97.7	5145	20	US-10-357-930-22820	Sequence 22820, A
25	2606	97.7	5145	20	US-10-357-930-26669	Sequence 26669, A
26	2606	97.7	5145	20	US-10-357-930-26815	Sequence 26815, A
27	2606	97.7	5145	20	US-10-357-930-26912	Sequence 26912, A
28	2606	97.7	5145	20	US-10-357-930-26923	Sequence 26923, A
29	2606	97.7	5145	20	US-10-357-930-27145	Sequence 27145, A
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31	2606	97.7	5145	20	US-10-357-930-28675	Sequence 28675, A
32	2594	97.2	5450	22	US-10-029-345A-108	Sequence 108, App
33	2594	97.2	5450	22	US-10-029-345A-147	Sequence 147, App
34	2588	97.0	5111	22	US-10-029-345A-41	Sequence 41, Appl
35	2580.5	96.7	2200	18	US-10-072-012-255	Sequence 255, App
36	2579.5	96.7	2071	18	US-10-072-012-257	Sequence 257, App
37	2259.5	84.7	2756	22	US-10-029-345A-113	Sequence 113, App
38	1643.5	61.6	1916	17	US-10-108-260A-2429	Sequence 2429, Ap
39	844	31.6	2377	21	US-10-278-698-169	Sequence 169, App
40	844	31.6	2377	21	US-10-278-698-685	Sequence 685, App
41	823	30.8	2453	13	US-10-005-858-1	Sequence 1, Appli
42	809	30.3	2476	18	US-10-220-120-28	Sequence 28, Appl
c 43	707	26.5	425	20	US-10-357-930-10717	Sequence 10717, A
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c 45	703	26.3	467	20	US-10-357-930-40868	Sequence 40868, A

ALIGNMENTS

RESULT 1
US-09-964-277-20
; Sequence 20, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 3332
; TYPE: DNA

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;   ORGANISM: Homo sapiens
US-09-964-277-20

Alignment Scores:
Pred. No.:              5.53e-257       Length:         3332
Score:                  2668.00         Matches:        517
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-964-277-21 (1-517) x US-09-964-277-20 (1-3332)

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Qy         41 LeuAsnAlaSerAsnThrCysProLysProAspPheIleProGluSerHisPheLeuArg 60
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Qy         81 PheIleGluLysAlaLysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIle 100
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Qy        341 ThrSerSerSerGlyThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySer 360
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Qy        381 ThrLysSerAlaGlyLeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThr 400
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Qy        401 SerThrProSerLeuThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSer 420
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Qy        461 SerArgArgSerTrpHisGluGluSerProPheGluLysGlnPheLysArgArgSerCys 480
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RESULT 2
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel A.
;  TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
;  TITLE OF INVENTION:  PHOSPHATASE MOLECULES AND USES THEREFOR
;  FILE REFERENCE: 10448-030002
;  CURRENT APPLICATION NUMBER: US/09/816,494
;  CURRENT FILING DATE:  2001-03-23
;  PRIOR APPLICATION NUMBER: US 60/191,858
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1998
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-816-494-3

Alignment Scores:
Pred. No.:              4.43e-251       Length:         1998
Score:                  2606.00         Matches:        516
Percent Similarity:     90.21%          Conservative:   0
Best Local Similarity:  90.21%          Mismatches:     1
Query Match:            97.68%          Indels:         56
DB:                     9               Gaps:           1
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US-09-964-277-21 (1-517) x US-09-816-494-3 (1-1998)

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Qy         21 AlaSerThrLeuPheThrCysLeuGln-------------------------------- 29
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Db        520 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 579

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
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Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
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Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
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Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
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Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
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Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
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Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
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Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
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Db       1180 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1239

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
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Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
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Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
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Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
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Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
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Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
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Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1840 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 1899

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1900 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 1959

Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
              |||||||||||||||||||||||||||||||||||
Db       1960 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 1995
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RESULT 3
US-10-377-072-27
; Sequence 27, Application US/10377072
; Publication No. US20040009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MPI03-018OMNIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07

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;  PRIOR APPLICATION NUMBER: US 09/843,297
;  PRIOR FILING DATE: 2001-04-25
;  PRIOR APPLICATION NUMBER: US 60/199,801
;  PRIOR FILING DATE: 2000-04-26
;  PRIOR APPLICATION NUMBER: US 09/861,801
;  PRIOR FILING DATE: 2001-05-21
;  PRIOR APPLICATION NUMBER: US 60/205,508
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 09/816,494
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: US 09/815,419
;  PRIOR FILING DATE: 2001-03-22
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 1998
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1998)
US-10-377-072-27

Alignment Scores:
Pred. No.:              4.43e-251      Length:          1998
Score:                  2606.00        Matches:         516
Percent Similarity:     90.21%         Conservative:    0
Best Local Similarity:  90.21%         Mismatches:      1
Query Match:            97.68%         Indels:          56
DB:                     17             Gaps:            1

US-09-964-277-21 (1-517) x US-10-377-072-27 (1-1998)

Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 340

Qy         21 AlaSerThrLeuPheThrCysLeuGln---------------------------------- 29
              |||||||||||||||||||||||||
Db        341 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 399

Qy         29 ------------------------------------------------------------ 29

Db        400 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 459

Qy         29 ------------------------------------------------------------ 29

Db        460 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 519

Qy         30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 579

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 639

Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 699

Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 759

Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 819

Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 879

Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 939

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 999

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1059

Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1119

Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1179

Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1180 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1239

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1299

Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1300 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1359

Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1360 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 1419

Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1420 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 1479

Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1480 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 1539

Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1540 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 1599

Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1600 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 1659

Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1660 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 1719

Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1720 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 1779

Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1780 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 1839

Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1840 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 1899

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1900 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 1959
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Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
              ||||||||||||||||||||||||||||||||||||
Db       1960 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 1995

RESULT 4
US-10-377-072-27
; Sequence 27, Application US/10377072
; Publication No. US20040157221A9
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals Inc.
;  APPLICANT:  Curtis, Rory A.J.
;  APPLICANT:  Logan, Thomas Joseph
;  APPLICANT:  Glucksmann, Maria A.
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  Williamson, Mark J.
;  APPLICANT:  Rudolph-Owen, Laura A.
;  APPLICANT:  Chun, Miyoung
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
;  TITLE OF INVENTION:  38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: MPI03-018OMNIM
;  CURRENT APPLICATION NUMBER: US/10/377,072
;  CURRENT FILING DATE:  2003-02-27
;  PRIOR APPLICATION NUMBER: US 09/895,860
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/215,370
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: US 09/723,806
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: US 60/187,455
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 09/843,297
;  PRIOR FILING DATE: 2001-04-25
;  PRIOR APPLICATION NUMBER: US 60/199,801
;  PRIOR FILING DATE: 2000-04-26
;  PRIOR APPLICATION NUMBER: US 09/861,801
;  PRIOR FILING DATE: 2001-05-21
;  PRIOR APPLICATION NUMBER: US 60/205,508
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 09/816,494
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: US 09/815,419
;  PRIOR FILING DATE: 2001-03-22
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 1998
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1998)
US-10-377-072-27

Alignment Scores:
Pred. No.:              4.43e-251      Length:          1998
Score:                  2606.00        Matches:         516
Percent Similarity:     90.21%         Conservative:    0
Best Local Similarity:  90.21%         Mismatches:      1
Query Match:            97.68%         Indels:          56
DB:                     19             Gaps:            1

US-09-964-277-21 (1-517) x US-10-377-072-27 (1-1998)

Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 340

Qy         21 AlaSerThrLeuPheThrCysLeuGln-------------------------------- 29
              |||||||||||||||||||||||||
Db        341 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 399

Qy         29 ------------------------------------------------------------ 29

Db        400 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 459

Qy         29 ------------------------------------------------------------ 29

Db        460 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 519

Qy         30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
                          ||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 579

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 639

Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 699

Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 759

Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 819

Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 879

Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 939

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 999

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1059

Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1119

Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1179

Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1180 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1239

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1299

Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1300 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1359

Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1360 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 1419

Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1420 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 1479
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Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1480 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 1539

Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1540 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 1599

Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1600 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 1659

Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1660 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 1719

Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1720 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 1779

Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1780 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 1839

Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1840 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 1899

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1900 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 1959

Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
              |||||||||||||||||||||||||||||||||||
Db       1960 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 1995

RESULT 5
US-10-094-749-673
; Sequence 673, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
;  FILE REFERENCE: 084335/0160
;  CURRENT APPLICATION NUMBER: US/10/094,749
;  CURRENT FILING DATE:  2002-03-12
;  PRIOR APPLICATION NUMBER: 60/350,435
;  PRIOR FILING DATE: 2002-01-24
;  PRIOR APPLICATION NUMBER: JP 2001-328381
;  PRIOR FILING DATE: 2001-09-14
;  NUMBER OF SEQ ID NOS: 3381
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 673
;   LENGTH: 2102
;   TYPE: DNA
;   ORGANISM: Homo sapiens

US-10-094-749-673

Alignment Scores:
Pred. No.:                4.77e-251      Length:          2102
Score:                    2606.00        Matches:         516
Percent Similarity:       90.21%         Conservative:    0
Best Local Similarity:    90.21%         Mismatches:      1
Query Match:              97.68%         Indels:          56
DB:                       17             Gaps:            1

US-09-964-277-21 (1-517) x US-10-094-749-673 (1-2102)

Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 395

Qy         21 AlaSerThrLeuPheThrCysLeuGln---------------------------------- 29
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Db        396 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 454

Qy         29 ---------------------------------------------------------- 29

Db        455 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 514

Qy         29 ---------------------------------------------------------- 29

Db        515 GTTGCCAACATTGGGCCAACCCTAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 574

Qy         30 -----------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
                         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 634

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 694

Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 754

Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 814

Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        815 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 874

Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 GTGAAAGAAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 934

Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        935 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 994

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        995 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1054

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1055 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1114

Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1115 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1174

Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1175 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1234

Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1235 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1294

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1295 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1354

Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1355 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1414

Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1415 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACT 1474

Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1475 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 1534

Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1535 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 1594

Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1595 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 1654

Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1655 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 1714

Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1715 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 1774

Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1775 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 1834

Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1835 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 1894

Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1895 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 1954

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1955 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2014

Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
                |||||||||||||||||||||||||||||||||||
Db       2015 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2050

RESULT 6
US-10-168-506-2
; Sequence 2, Application US/10168506
; Publication No. US20040053229A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY D.
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  SUDARSANAM, SUCHA
;  APPLICANT:  HILL, RON
;  APPLICANT:  FLANAGAN, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: 038602/1351
;  CURRENT APPLICATION NUMBER: US/10/168,506
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: PCT/US00/34736
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 2732
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-168-506-2

Alignment Scores:
Pred. No.:              7e-251          Length:         2732
Score:                  2606.00         Matches:        516
Percent Similarity:     90.21%          Conservative:   0
Best Local Similarity:  90.21%          Mismatches:     1
Query Match:            97.68%          Indels:         56
DB:                     18              Gaps:           1

US-09-964-277-21 (1-517) x US-10-168-506-2 (1-2732)

Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        818 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 877

Qy         21 AlaSerThrLeuPheThrCysLeuGln-------------------------------- 29
                |||||||||||||||||||||||||
Db        878 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 936

Qy         29 ---------------------------------------------------------- 29

Db        937 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 996

Qy         29 ---------------------------------------------------------- 29

Db        997 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 1056

Qy         30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1057 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 1116

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 1176

Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 1236

Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1296

Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1297 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1356

Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1357 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1416

Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
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Db       1417 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1476

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1477 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1536

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1537 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1596

Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1597 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1656
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Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1657 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1716

Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1717 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1776

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1777 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1836

Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1837 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1896

Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1897 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACT 1956

Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1957 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 2016

Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2017 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 2076

Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2077 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 2136

Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2137 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 2196

Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2197 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 2256

Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2257 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 2316

Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2317 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 2376

Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2377 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2436

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2437 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2496

Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
              |||||||||||||||||||||||||||||||||||
Db       2497 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2532

RESULT 7
US-10-838-181-2
; Sequence 2, Application US/10838181
; Publication No. US20050084877A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY D.
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  SUDARSANAM, SUCHA
;  APPLICANT:  HILL, RON
;  APPLICANT:  FLANAGAN, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: 038602/1351
;  CURRENT APPLICATION NUMBER: US/10/838,181
;  CURRENT FILING DATE:  2004-05-04
;  PRIOR APPLICATION NUMBER: US/10/168,506
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: PCT/US00/34736
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 2732
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-838-181-2

Alignment Scores:
Pred. No.:              7e-251          Length:         2732
Score:                  2606.00         Matches:        516
Percent Similarity:     90.21%          Conservative:   0
Best Local Similarity:  90.21%          Mismatches:     1
Query Match:            97.68%          Indels:         56
DB:                     21              Gaps:           1

US-09-964-277-21 (1-517) x US-10-838-181-2 (1-2732)

Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        818 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 877

Qy         21 AlaSerThrLeuPheThrCysLeuGln-------------------------------- 29
              |||||||||||||||||||||||||
Db        878 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 936

Qy         29 ------------------------------------------------------------ 29

Db        937 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 996

Qy         29 ------------------------------------------------------------ 29

Db        997 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 1056

Qy         30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1057 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 1116

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 1176

Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 1236

Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1296

Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1297 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1356

Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1357 GTGAAAGAAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1416

Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1417 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1476

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1477 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1536
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Qy       186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db      1537 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1596

Qy       206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
Db      1597 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1656

Qy       226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
Db      1657 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1716

Qy       246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
Db      1717 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1776

Qy       266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
Db      1777 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1836

Qy       286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
Db      1837 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1896

Qy       306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
Db      1897 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACT 1956

Qy       326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
Db      1957 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 2016

Qy       346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
Db      2017 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 2076

Qy       366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
Db      2077 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 2136

Qy       386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db      2137 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 2196

Qy       406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
Db      2197 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 2256

Qy       426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
Db      2257 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 2316

Qy       446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
Db      2317 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 2376

Qy       466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
Db      2377 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2436

Qy       486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
Db      2437 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2496

Qy       506 SerPheSerGlySerMetGluIleIleGluValSer 517
Db      2497 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2532

RESULT 8
US-10-296-115-520
; Sequence 520, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq Inc
;  TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 784PCT
;  CURRENT APPLICATION NUMBER: US/10/296,115
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: US09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 520
;   LENGTH: 2966
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(2966)
;   OTHER INFORMATION: n = a,t,c or g
US-10-296-115-520

Alignment Scores:
Pred. No.:                7.89e-251       Length:          2966
Score:                    2606.00         Matches:         516
Percent Similarity:       90.21%          Conservative:    0
Best Local Similarity:    90.21%          Mismatches:      1
Query Match:              97.68%          Indels:          56
DB:                       18              Gaps:            1

US-09-964-277-21 (1-517) x US-10-296-115-520 (1-2966)

Qy         1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
Db       303 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 362

Qy        21 AlaSerThrLeuPheThrCysLeuGln---------------------------------- 29
Db       363 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 421

Qy        29 ------------------------------------------------------------ 29
Db       422 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 481

Qy        29 ------------------------------------------------------------ 29
Db       482 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 541

Qy        30 ----------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
Db       542 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 601

Qy        46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
Db       602 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 661

Qy        66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
Db       662 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 721

Qy        86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db       722 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 781

Qy       106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
Db       782 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 841

Qy       126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
Db       842 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 901

Qy       146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
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Db        902 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 961

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1021

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1081

Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1141

Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1201

Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1261

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1321

Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1381

Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 1441

Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 1501

Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 1561

Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 1621

Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 1681

Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 1741

Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 1801

Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1802 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 1861

Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1862 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 1921

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1922 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 1981

Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
              |||||||||||||||||||||||||||||||||||
Db       1982 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2017
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RESULT 9
US-10-257-026-1
; Sequence 1, Application US/10257026
; Publication No. US20040086859A1
; GENERAL INFORMATION:
;  APPLICANT: Merck Patent GmbH
;  TITLE OF INVENTION: New dual specificity phosphatase
;  FILE REFERENCE: DUSP10KDWS
;  CURRENT APPLICATION NUMBER: US/10/257,026
;  CURRENT FILING DATE:  2003-11-07
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3059
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (127)..(2121)
US-10-257-026-1

Alignment Scores:
Pred. No.:              8.26e-251       Length:         3059
Score:                  2606.00         Matches:        516
Percent Similarity:     90.21%          Conservative:   0
Best Local Similarity:  90.21%          Mismatches:     1
Query Match:            97.68%          Indels:         56
DB:                     18              Gaps:           1

US-09-964-277-21 (1-517) x US-10-257-026-1 (1-3059)

Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 466

Qy         21 AlaSerThrLeuPheThrCysLeuGln-------------------------------- 29
              |||||||||||||||||||||||||
Db        467 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 525

Qy         29 ------------------------------------------------------------ 29

Db        526 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 585

Qy         29 ------------------------------------------------------------ 29

Db        586 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 645

Qy         30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 705

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 765

Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 825

Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 885

Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 945

Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1005

Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
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Db       1006 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1065

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185

Db       1066 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1125

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205

Db       1126 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1185

Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225

Db       1186 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1245

Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245

Db       1246 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1305

Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265

Db       1306 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1365

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285

Db       1366 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1425

Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305

Db       1426 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1485

Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325

Db       1486 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 1545

Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345

Db       1546 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 1605

Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365

Db       1606 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 1665

Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385

Db       1666 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 1725

Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405

Db       1726 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 1785

Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425

Db       1786 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 1845

Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445

Db       1846 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 1905

Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465

Db       1906 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 1965

Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485

Db       1966 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2025

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505

Db       2026 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2085

Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517

Db       2086 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2121

RESULT 10
US-09-964-277-1
; Sequence 1, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
;  APPLICANT: Luche, Ralf M.
;  APPLICANT:  Wei, Bo
;  TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
;  FILE REFERENCE: 200125.434
;  CURRENT APPLICATION NUMBER: US/09/964,277
;  CURRENT FILING DATE:  2001-09-25
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3496
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-964-277-1

Alignment Scores:
Pred. No.:                1e-250          Length:          3496
Score:                    2606.00         Matches:         516
Percent Similarity:       90.21%          Conservative:    0
Best Local Similarity:    90.21%          Mismatches:      1
Query Match:              97.68%          Indels:          56
DB:                       9               Gaps:            1

US-09-964-277-21 (1-517) x US-09-964-277-1 (1-3496)

Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20

Db        842 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 901

Qy         21 AlaSerThrLeuPheThrCysLeuGln---------------------------------- 29

Db        902 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 960

Qy         29 ---------------------------------------------------------- 29

Db        961 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 1020

Qy         29 ---------------------------------------------------------- 29

Db       1021 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 1080

Qy         30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45

Db       1081 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 1140

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65

Db       1141 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 1200

Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85

Db       1201 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 1260

Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105

Db       1261 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1320

Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125

Db       1321 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1380

Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145

Db       1381 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1440

Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
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Db       1441 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1500

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1560

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1620

Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1680

Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1740

Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1800

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1860

Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1920

Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 1980

Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 2040

Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 2100

Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 2160

Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 2220

Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 2280

Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 2340

Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 2400

Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2460

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2520

Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
              |||||||||||||||||||||||||||||||||||||
Db       2521 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2556
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RESULT 11
US-10-370-715B-261
; Sequence 261, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
;    Patin Docket Preview
;  APPLICANT: BODARY,SARAH C.
;  APPLICANT:  CLARK,HILLARY
;  APPLICANT:  BRISDELL,HUNTE
;  APPLICANT:  JACKMAN,JANET
;  APPLICANT:  SCHOENFELD,JILL R.
;  APPLICANT:  WILLIAMS,P. MICKEY
;  APPLICANT:  WOOD,WILLIAM I.
;  APPLICANT:  WU,THOMAS D.
;  TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
;  TITLE OF INVENTION:  Related Diseases
;  FILE REFERENCE: P1948R1-US
;  CURRENT APPLICATION NUMBER: US/10/370,715B
;  CURRENT FILING DATE:  2003-02-21
;  NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 261
;   LENGTH: 3521
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-370-715B-261

Alignment Scores:
Pred. No.:              1.01e-250      Length:          3521
Score:                  2606.00        Matches:         516
Percent Similarity:     90.21%         Conservative:    0
Best Local Similarity:  90.21%         Mismatches:      1
Query Match:            97.68%         Indels:          56
DB:                     20             Gaps:            1

US-09-964-277-21 (1-517) x US-10-370-715B-261 (1-3521)

Qy           1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         844 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 903

Qy          21 AlaSerThrLeuPheThrCysLeuGln-------------------------------- 29
               |||||||||||||||||||||||||
Db         904 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 962

Qy          29 ---------------------------------------------------------- 29

Db         963 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 1022

Qy          29 ---------------------------------------------------------- 29

Db        1023 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 1082

Qy          30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
                           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1083 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 1142

Qy          46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1143 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 1202

Qy          66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1203 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 1262

Qy          86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1263 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1322

Qy         106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1323 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1382
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Qy       126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
Db      1383 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1442

Qy       146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
Db      1443 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1502

Qy       166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
Db      1503 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1562

Qy       186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db      1563 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1622

Qy       206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
Db      1623 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1682

Qy       226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
Db      1683 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1742

Qy       246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
Db      1743 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1802

Qy       266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
Db      1803 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1862

Qy       286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
Db      1863 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1922

Qy       306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
Db      1923 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 1982

Qy       326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
Db      1983 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 2042

Qy       346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
Db      2043 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 2102

Qy       366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
Db      2103 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 2162

Qy       386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db      2163 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 2222

Qy       406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
Db      2223 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 2282

Qy       426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
Db      2283 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 2342

Qy       446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
Db      2343 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 2402

Qy       466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
Db      2403 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2462

Qy       486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
Db      2463 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2522

Qy       506 SerPheSerGlySerMetGluIleIleGluValSer 517
Db      2523 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2558
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RESULT 12
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2583)
US-09-816-494-1

Alignment Scores:

Pred. No.:	1.02e-250	Length:	3544
Score:	2606.00	Matches:	516
Percent Similarity:	90.21%	Conservative:	0
Best Local Similarity:	90.21%	Mismatches:	1
Query Match:	97.68%	Indels:	56
DB:	9	Gaps:	1

US-09-964-277-21 (1-517) x US-09-816-494-1 (1-3544)

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Qy         1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
Db       869 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 928

Qy        21 AlaSerThrLeuPheThrCysLeuGln---------------------------------- 29
Db       929 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 987

Qy        29 ------------------------------------------------------------ 29
Db       988 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 1047

Qy        29 ------------------------------------------------------------ 29
Db      1048 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 1107

Qy        30 ----------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
Db      1108 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 1167

Qy        46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
Db      1168 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 1227

Qy        66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
Db      1228 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 1287

Qy        86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db      1288 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1347
```

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Qy       106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
Db      1348 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1407

Qy       126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
Db      1408 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1467

Qy       146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
Db      1468 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1527

Qy       166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
Db      1528 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1587

Qy       186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db      1588 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1647

Qy       206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
Db      1648 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1707

Qy       226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
Db      1708 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1767

Qy       246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
Db      1768 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1827

Qy       266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
Db      1828 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1887

Qy       286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
Db      1888 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1947

Qy       306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
Db      1948 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 2007

Qy       326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
Db      2008 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 2067

Qy       346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
Db      2068 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 2127

Qy       366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
Db      2128 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 2187

Qy       386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db      2188 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 2247

Qy       406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
Db      2248 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 2307

Qy       426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
Db      2308 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 2367

Qy       446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
Db      2368 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 2427

Qy       466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
Db      2428 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2487

Qy       486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
Db      2488 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2547

Qy       506 SerPheSerGlySerMetGluIleIleGluValSer 517
Db      2548 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2583
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RESULT 13
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MPI03-018OMNIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2586)
US-10-377-072-25

Alignment Scores:

Pred. No.:	1.02e-250	Length:	3544
Score:	2606.00	Matches:	516
Percent Similarity:	90.21%	Conservative:	0
Best Local Similarity:	90.21%	Mismatches:	1
Query Match:	97.68%	Indels:	56
DB:	17	Gaps:	1

US-09-964-277-21 (1-517) x US-10-377-072-25 (1-3544)

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Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 928

Qy         21 AlaSerThrLeuPheThrCysLeuGln------------------------------- 29
              |||||||||||||||||||||||||
Db        929 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 987

Qy         29 ------------------------------------------------------------ 29

Db        988 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 1047

Qy         29 ------------------------------------------------------------ 29

Db       1048 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 1107

Qy         30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 1167

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 1227

Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1228 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 1287

Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1288 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1347

Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1348 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1407

Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1408 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1467

Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1468 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1527

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1528 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1587

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1588 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1647

Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1648 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1707

Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1708 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1767

Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1768 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1827

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1828 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1887

Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1888 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1947

Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1948 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 2007

Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2008 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 2067

Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2068 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 2127

Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2128 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 2187

Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 2247

Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 2307

Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2308 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 2367

Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2368 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 2427

Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2428 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2487

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2488 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2547

Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
              |||||||||||||||||||||||||||||||||||
Db       2548 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2583
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RESULT 14
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040157221A9
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MPI03-018OMNIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25

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;  PRIOR APPLICATION NUMBER: US 60/199,801
;  PRIOR FILING DATE: 2000-04-26
;  PRIOR APPLICATION NUMBER: US 09/861,801
;  PRIOR FILING DATE: 2001-05-21
;  PRIOR APPLICATION NUMBER: US 60/205,508
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 09/816,494
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: US 09/815,419
;  PRIOR FILING DATE: 2001-03-22
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 3544
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (589)...(2586)
US-10-377-072-25

Alignment Scores:
Pred. No.:              1.02e-250      Length:         3544
Score:                  2606.00        Matches:        516
Percent Similarity:     90.21%         Conservative:   0
Best Local Similarity:  90.21%         Mismatches:     1
Query Match:            97.68%         Indels:         56
DB:                     19             Gaps:           1

US-09-964-277-21 (1-517) x US-10-377-072-25 (1-3544)

Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 928

Qy         21 AlaSerThrLeuPheThrCysLeuGln---------------------------------- 29
              |||||||||||||||||||||||||
Db        929 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 987

Qy         29 ------------------------------------------------------------ 29

Db        988 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 1047

Qy         29 ------------------------------------------------------------ 29

Db       1048 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 1107

Qy         30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 1167

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 1227

Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1228 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 1287

Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1288 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1347

Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1348 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1407

Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1408 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1467

Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1468 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1527

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1528 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1587

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1588 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1647

Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1648 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1707

Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1708 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1767

Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1768 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1827

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1828 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1887

Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1888 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 1947

Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1948 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 2007

Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2008 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 2067

Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2068 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 2127

Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2128 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 2187

Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 2247

Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 2307

Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2308 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 2367

Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2368 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 2427

Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2428 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2487

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2488 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2547

Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
              |||||||||||||||||||||||||||||||||||
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Db       2548 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2583

RESULT 15
US-10-425-114-26234
; Sequence 26234, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26234
;   LENGTH: 3625
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
US-10-425-114-26234

Alignment Scores:
Pred. No.:              1.06e-250      Length:          3625
Score:                  2606.00        Matches:         516
Percent Similarity:     90.21%         Conservative:    0
Best Local Similarity:  90.21%         Mismatches:      1
Query Match:            97.68%         Indels:          56
DB:                     18             Gaps:            1

US-09-964-277-21 (1-517) x US-10-425-114-26234 (1-3625)

Qy          1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGA 1031

Qy         21 AlaSerThrLeuPheThrCysLeuGln---------------------------------- 29
              |||||||||||||||||||||||||
Db       1032 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCT 1090

Qy         29 ---------------------------------------------------------- 29

Db       1091 GGCCTCTGTGAAGGAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 1150

Qy         29 ---------------------------------------------------------- 29

Db       1151 GTTGCCAACATTGGGCCAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 1210

Qy         30 ------------GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1211 GTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATGTGTTAAATGCCAGCAAT 1270

Qy         46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGAC 1330

Qy         66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1331 AGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCA 1390

Qy         86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1391 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1450

Qy        106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1451 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1510

Qy        126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1511 GTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1570

Qy        146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1571 TATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1630

Qy        166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1631 CTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC 1690

Qy        186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1691 GAGACGCCCCTCAGTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGG 1750

Qy        206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1751 CCCGTGCATCCCGCCAGCGTGCCCAGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGAC 1810

Qy        226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1811 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGC 1870

Qy        246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1871 AATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCATG 1930

Qy        266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1931 GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1990

Qy        286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1991 ACTACTCTGGATGGGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAG 2050

Qy        306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2051 CAGACTCCCGAAACCAGTCCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 2110

Qy        326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2111 GCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCAGCAGCAGTGGC 2170

Qy        346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2171 ACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 2230

Qy        366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2231 CACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGC 2290

Qy        386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2291 CTGGGCCTTAAGGGCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTG 2350

Qy        406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2351 ACCAGCAGCTGGTATTTTGCCACAGAGTCCTCACACTTCTACTCTGCCTCAGCCATCTAC 2410

Qy        426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2411 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGCCCACTTGCGGAGACCAA 2470

Qy        446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2471 GTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGG 2530

Qy        466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2531 CATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGA 2590

Qy        486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2591 GAGAGCATCATGTCAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2650

Qy        506 SerPheSerGlySerMetGluIleIleGluValSer 517
              |||||||||||||||||||||||||||||||||||
Db       2651 AGCTTTTCGGGCAGCATGGAAATCATTGAGGTCTCC 2686


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Job time : 989 secs
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